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# Quality Evaluations of Hard Red Spring Wheat Grown in South Dakota

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# QUALITY EVALUATIONS OF HARD RED SPRING WHEAT GROWN IN SOUTH DAKOTA

BY

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This thesis is approved as a creditable and independent investigation by a candidate for the Master of Science in Plant Science degree and is acceptable for meeting the thesis requirements for this degree. Acceptance of this does not imply that the conclusions reached by the candidate are necessarily the conclusions of the major department.

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This thesis is dedicated to my mother.

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CONTENTS

# ABBREVIATIONS

AACC: American Association of Cereal Chemists

ABS: water absorption

AEA: average environment axis

AEC: average environment coordination

AMMI: additive main effect and multiplicative interaction

ASH: ash content

AUP: adjusted unbiased prediction approach

BU: bushel

DGC: dry gluten content

ELS: top-of-envelope left-of-peak slope

EPT: top-of-envelope peak time

EPV: top-of-envelope peak value

ERS: top-of-envelope right-of-peak slope

ET: environment-by-trait

EXT: flour extraction

FGIS: Federal Grain Inspection Service

FPC: flour protein content

G: genotype

GE: genotype-by-environment

GGL: genotype-by-genotype x location

GGE: genotype-by-genotype x environment

GGS: genotype-by-subregion

GI: gluten index

GL: genotype-by-location

GLY: genotype-by-location-by-year

GPC: grain protein content

GT: genotype-by-trait

GY: genotype-by-year

Hl: hectare

HRS: Hard Red Spring

HRSW: Hard Red Spring Wheat

HRW: Hard Red Winter

HW: Hard White

Kg: kilogram

L: location

LMM: Linear mixed model

LT: location-by-trait

MINQUE: minimum norm quadratic unbiased estimation

ML: maximum likelihood

MLS: mid-line left-of-peak slope

MPT: mid-line variables peak time

MPV: mid-line peak value

MSE: top-of-envelope mixing stability

MSM: mid-line mixing stability

MRS: mid-line right-of-peak slope

N: Sample Size

NASS: National Agricultural Statistics Service

NIR: Near-Infrared Reflectance

PC: principal components

RDM: recording dough mixer

REML: restricted maximum likelihood

SRW: Soft Red Winter

SS: sum of squares

SVD: singular value decomposition

SW: Soft White

TKW: thousand kernel weight

TWT: test weight

USDA: United States Department of Agriculture

WB: water-binding

WGC: wet gluten content

Y: year

YT: year-by-trait

# LIST OF FIGURES

# LIST OF TABLES

# ABSTRACT

QUALITY EVALUATIONS OF HARD RED SPRING WHEAT
VARIETIES GROWN IN SOUTH DAKOTA

LANCE MERRICK

2019

Hard Red Spring Wheat (HRSW; *Triticum aestivum* L.) is characterized by generally high protein content and excellent baking and milling performance. The ability for millers, bakers, and other end-users of wheat to properly and cheaply produce food products with uniformity is dependent on the quality consistency of wheat produced by breeders and farmers. Determining how production years and locations influenced end-use quality traits will assist breeders, agronomists, and growers, in understanding which hard red spring wheat (HRSW; *Triticum aestivum* L.) varieties are least susceptible to quality fluctuations, and therefore, most desirable to end-users. In order to determine which varieties were more consistent in certain locations, analyses on how end-use quality fluctuates in specific locations were conducted.

The analyses were completed on an unbalanced dataset represented by one thousand four hundred and twenty-three HRSW samples. These samples were from seven years and thirty-eight counties throughout South Dakota comprised of twelve varieties and were evaluated for twenty-one traits and variables from common screening methods. The averages and trends for each trait for the varieties, counties, and years were reported.

To overcome the analytical challenges with incomplete datasets, Pearson correlation coefficients, variance component estimation and heritability using a genotype-

by-location-by year (GLY) linear mixed model, along with biplot analysis for mega-environment evaluation using singular value decomposition (SVD) analysis were completed for 21 end-use quality traits.

Predicted estimates from the adjusted unbiased prediction approach (AUP) and biplot analysis, determined that Briggs, Steele-ND, and Barlow varieties resulted in the best end-use quality wheat for most of the counties represented in South Dakota. This study also revealed the higher end-use quality, in regard to protein, gluten, and rheological traits, effect for counties in the North Central and North West USDA crop reporting districts in South Dakota, in particularly Faulk, Beadle, and Hutchinson. The results of the combination of biplots and variance component estimation is that traits are more variable between years and varieties as compared to the counties. This indicates that specific county effects are not large enough to ignore the importance of selecting the proper variety and testing it in multiple years.

# CHAPTER 1: LITERATURE REVIEW

## I. INTRODUCTION

### A. WHEAT ORIGIN AND USES

Wheat, *Triticum* spp., is a major food and crop for humans and the first sign of domestication appeared over 10,000 years ago in the Fertile Crescent. The domestication was rapid and focused on selection for non-shattering, free-threshing spikelets and for higher yield. The domestication of cereals was essential for agriculture-based societies which lead to urbanization and large population growth (Carver, 2009).

Modern wheat primarily consists of hexaploidy bread wheat, *Triticum aestivum* L., and its genetic diversity is comprised of over 25,000 different cultivars and is referred to as 'common wheat'. Hexaploid wheat was derived from the hybridization of tetraploid wheat with genomes (BBAA) and a diploid wheat with genome (DD). Hexaploid wheat still as similar inhertance to diploid species due to complete diploidlike chromosome pairing controlled by two main homoeologous pairing genes (Carver, 2009).

Wheat is the world's largest and most important food crop with more than 620 million tonnes from over 40 countries. The USA produces around 55 to 60 million tonnes per year and supplies about 40% of the world's exports. Wheat is an important dietary component and is a major source of protein and attributes to over 55% of the world's carbohydrates. What makes wheat so unique is the gluten proteins in the endosperm that are responsible for wheat dough 's bread-baking qualities. This bread making ability has led wheat to be a staple food throughout history(Carver, 2009).

In an effort to meet population growth and demand, there has been a steady increase in yield. Despite this increase, there is a need to increase high-quality protein sources for areas of the world that still face protein deficiency such as in Asia and Africa that obtain around 80% of their protein from plants. The nutritional composition of wheat will become critical as the world wheat demand increases while wheat stocks decrease. This is in part due to the projected population of the world to reach 9.3 billion people by 2050. This will create a 66% increase in agricultural production by 2040 even as the amount of arable land continues to diminish. This creates a large need for the improvement of wheat production and quality (Carver, 2009).

However, increasing yield without negatively affecting the quality of the wheat and flour is difficult due to the negative correlation between yield and grain protein content. Generally, as yield increases, grain protein content decreases, which is strongly associated with bread-making quality or end-use quality. That is why breeders try to balance quality and yield traits when improving and developing cultivars (Curtis et al,, 2002).

## B. WHEAT CLASSIFICATION

In the USA, wheat is classified by the US Federal Grain Inspection Service (FGIS) under the US Department of Agriculture (USDA) into eight classifications (Carver, 2009). Wheat can be referred to as hard or soft depending on grain hardness. It can then be further classified by color and categorized as red or white (Curtis et al., 2002). The color is the most commonly used characteristic and describes the color of the outer layer of the kernel, also known as the bran coat (Carver, 2009). And finally, wheat

can be further divided into spring or winter wheat depending on its growth habit depending on the time it is planted and whether or not it requires vernalization. Six out of the eight classifications are economically important in the USA. These include, Hard Red Winter (HRW), Soft Red Winter (SRW), Hard Red Spring (HRS), Soft White (SW), Hard White (HW), and durum (Curtis et al., 2002).

Hard Red Spring wheat (HRSW) is classified by the hardness of the endosperm, hard, the color of the bran coat, red, and the growing cycle, spring. It is planted in spring and harvested in late summer. It is generally planted in areas with harsh winters with low temperatures. In the USA, it is mainly found in the northern plains and is one of main classification of wheat used for baking bread. It has a high protein content and gluten quality that makes it stand out compared to other classifications of wheat. It is used for breads made with yeast, hearth breads, whole grain breads, and pizza crusts. Flour mills use HRSW as a blending wheat to increase gluten strength in batches of flour. This increases dough and mixing properties (U.S. Wheat Associates, 2017).

## C. YIELD AND STATISTICS IN SD

In 2017 in South Dakota, HRSW was planted in 970,000 acres and 670,000 acres was harvested at an average of 31 bushels/acre. There was an increase in 2018, HRSW was planted in 1,050,000 acres and 965,000 acres was harvested at an average of 42 bushels/acre according to the USDA National Agricultural Statistics Service (NASS) (www.nass.usda.gov). In South Dakota there are 9 USDA crop reporting districts, which are contained in a map in figure 1.1, and their production statistics in table 1.1. These include Central, East Central, North Central, North East, North West, South Central,

South West, South east, and West Central districts. The top producing district in South Dakota in 2018 was the North Central district with 326,500 acres planted and 319,000 acres harvested with an average yield of 44.9 bushels/acre. The next highest producing districts in South Dakota had 100,000 less acres, which showed there is massive potential for the increase in acreage and production for spring wheat within the spring wheat producing areas of South Dakota.

# II. END-USE QUALITY

Wheat is graded into five grades numbered one through five. The important factors include foreign material, shrunken, broken, damaged, and defected kernels are important due to the negative affects they have on quality of the flour yielded. Test weight is also reported in kg/hl. However, these grading factors characterize wheat in relation to milling quality but do not grade the quality or end-use performance of the flour. Quality is considered a non-grade factor but influences the value and outcomes for the buyers and millers. Common non-grade quality factors can include moisture, protein, ash content, enzyme activity, dough characteristics and baking characteristics. Millers and bakers place emphasis into these non-grade factors even though they are not included in the FGIS grading system (Carver, 2009).

## A. KERNEL QUALITY

Kernel quality, also known as grain quality has many grade and non-grade factors. All of the grade factors discussed previously are based off of kernel quality. However, when it comes to quality, the kernel non-grade factors are the best indication of wheat

end-use quality and bread-making potential. Below are the most extensively used and measured in breeding programs due to high-throughput capabilities. Test weight, thousand kernel weight, and most importantly, protein content are very important traits that can be measured without the need for milling flour or baking bread.

## i. GRAIN PROTEIN

Grain protein content (GPC) depends heavily on genetics of the cultivar and the environment. It ranges from 8 to 17 percent. The amount of grain protein content can significantly influence the dough strength properties of a wheat variety. Content cannot explain the quality differences between cultivars, and therefore, the glutenin subunits must be taken into account (Curtis et al., 2002). Protein heritability is rather low compared to other quality traits. Furthermore, the selection for higher protein is complicated by a negative association with grain yield. Protein is one of the most important constituents of wheat. It is a significant factor in price determination. Protein content is an indicator of overall wheat quality.

## ii. TEST WEIGHT

Test weight (TWT) is one of the grading factors used by the US FGIS. It indicates better quality wheat and is correlated with easier processing and greater flour yield. Test weight does not necessarily translate into measurable milling yield. This is because test weight does not account for other important factors such as kernel uniformity, size, shape, and other environmental factors. It is usually measured in pounds per bushel in the US but in most of the world it is measured in kg/hl (Carver, 2009).

### iii. THOUSAND KERNEL WEIGHT

Thousand kernel weight (TKW) supplements test weight in determining flour yield due to the fact that grain samples with similar test weights may have differing thousand kernel weight. TKW is expressed as the weight in grams of 1,000 kernels. It is correlated to flour yield (Pomeranz & Hlynka, 1971). It is influenced by size and density of the wheat kernels but is less affected by environmental factors as compared to test weight (Carver, 2009).

## B. FLOUR QUALITY

Flour quality is the conformance to various measurable characteristics that are significant in terms of end use. Flour quality is the ability of the flour to produce a uniform, good end-use product defined by suppliers and buyers. Flour strength is an important aspect of quality due to the strength of the flour dictates the sustainability of the flour for specific end uses. There are many methods that evaluate flour strength that measure characteristics of the flour (Pomeranz & Hlynka, 1971). Flour quality can be measured by various tests that measure rheological and physical characteristics of the flour. It is difficult to evaluate the flour protein quality as compared to the flour protein content. Therefore, there are various methods used to measure the quality of the flour and culminates with various baking tests such as bread loaf volume (Pomeranz & Hlynka, 1971).

## i. FLOUR PROTEIN

Flour protein content (FPC) can be measured similarly to grain protein content by Kjeldahl digestion AACC Method, 46-10, 46-11A, 46-12, 46-13, the Dumas combustion AACC method, 46-30, and near-infrared reflectance (NIR) following the AACC Method, 39-00, 39-10, 39-11, and 39-25(American Association of Cereal Chemists. Approved Methods, 2000). Flour protein content is a major component of bread-making quality (Pomeranz & Hlynka, 1971).

## ii. FLOUR EXTRACTION

Milling yield is an extremely important characteristic for millers. This is because higher rates of flour extraction (EXT) result in higher financial returns from the same volume of grain (Peña et al., 2008). Flour extraction is the proportion of the wheat kernel that can be milled into flour. It is very important to mill profitability (U.S. Wheat Associates, 2017). It is expressed as a percentage of either the raw material used or the products obtained (Pomeranz & Hlynka, 1971).

## iii. FLOUR ASH CONTENT

Ash is the mineral residue present after incinerating a wheat or flour sample. Ash content (ASH) is expressed as a percentage at a given moisture basis. Millers need to know the amount of minerals present in a wheat sample because bakers have a maximum allowable mineral content of flour (Carver, 2009). The mineral content of flour is not necessarily related to the final performance of the flour (Pomeranz & Hlynka, 1971). Understanding the mineral content of the wheat allows millers to exclude the outermost

layers of the kernel where the mineral content is the highest and allows millers to increase the amount of flour extracted from the kernels and increase their profit margins (Carver, 2009).

### iv. GLUTEN

Gluten is a viscoelastic protein mass that forms as an insoluble protein in the presence of water. It is a unique and important property of wheat flour. Gluten comprises 75 to 85 percent of wheat endosperm protein. It is a large complex protein composed of polymeric and monomeric proteins known as glutenins and gliadins, respectively (Curtis et al., 2002). Glutenins are responsible for elasticity while gliadins are responsible for viscous flow and extensibility. Therefore, overall, gluten is responsible for most of the viscoelastic properties of the dough and is a major factor for determining the use of the dough for end-use products such as bread (Pomeranz & Hlynka, 1971).

## C. DOUGH QUALITY

Physical properties of doughs from different wheats are of major concern to bakers. Consistent dough properties are necessary for quality control of baked goods. Broad ranges in dough development, strength, elasticity, and extensibility are needed in baking for the various end-use products (Pomeranz & Hlynka, 1971).

### i. ABSORPTION

Dough absorption is correlated to flour moisture but depends on other factors. It is important in the production of most bake goods, and a higher absorption value is

generally desirable. It is measured as the amount of water required to yield a dough of a certain consistency. The absorption level is influenced by the gluten portion of flour and has a constant water-imbibing capacity whereas the water-soluble portion of the total protein content of the flour has no water-imbibing properties (Pomeranz & Hlynka, 1971).

## ii. RHEOLOGICAL PROPERTIES

Rheological properties of dough are important to the bakers. They determine the behavior of dough during mechanical handling and the quality of the finished bread. Dough is a mixture of flour, water, yeast, salt, and other ingredients and is an intermediate step in the process of transforming flour into bread. Rheological properties are based on the relationship between the stress on a material, which corresponds to the deformation or strain of it and time. Several tests can measure rheological properties of dough. They characterize the gluten portion of the protein by measuring extensibility and resistance to extension of dough at rest, hydration time, maximum development time, and tolerance to breakdown at a predetermined consistency during mixing. Recording dough mixers such as the mixograph, farinograph, extensograph, and alveograph evaluate the mixing characteristics of gluten development in dough. Mixing requirements are correlated with the measurements obtained with the recording dough mixers (Pomeranz & Hlynka, 1971).

### D. BREAD-MAKING QUALITY

Wheat bread provides more nutrients to the world population than any other food source. It serves as an inexpensive source of carbohydrates and proteins (Peña et al., 2008). Bread-making potential and quality is the culmination of all the quality traits and testing. Bread is the most common end-use product of HRSW, and all the quality tests try and measure important factors of wheat in its ability to make consistent bread. None of the tests can fully predict the bread-making quality and performance of the flour on their own. They serve as indexes that correlate to the final end-use product and can help predict the performance of the flour. The baking test is the final and ultimate test of quality of the flour. However, it requires a large volume of grain, baking facilities and are subjective in nature requiring well trained staff, making baking tests expensive. This process makes it difficult for a high-throughput screening method. Thus, the use of other various high-throughput testing methods that can test small amounts in a short period of time for certain quality traits and parameters and can be used to measure grain and flour quality and help predict bread-making potential (Pomeranz & Hlynka, 1971).

## III. BREEDING FOR END-USE QUALITY

The wheat industry requires several wheat types in order to satisfy the processing and quality requirements of different wheat-based products. The value of a wheat crop is determined by its grain attributes that satisfy specific end-use quality requirements (Peña et al., 2008). Along with higher yield, improved quality is a primary objective of most wheat breeders. However, due to a negative correlation between high yield and high protein, breeders find it difficult to obtain both (Khazratkulova et al., 2015). Since protein

is strongly associated with bread-making quality, breeders need to give protein and grain quality the same level of importance as yield and disease resistance. In order to develop cultivars, breeders need to understand the genetic control of quality traits, the relationship between quality traits and processing qualities, and achieve high-throughput rapid identification of quality traits by using quick, reliable, low-cost methodologies for testing quality.

## A. QUALITY TESTS

There are various tests used to measure quality, but the important ones used by plant breeders are high-throughput and help measure quality and the overall bread-making quality of the kernels and flour of wheat. The complex and additive nature of inheritance of most quality traits have led to the development of a range of indirect tests (Peña et al., 2008). These tests can be applied at all levels of the breeding process, and their ability to measure small samples allows the evaluation in early generations. This can make breeding programs more efficient by allowing breeders to discard inferior genotypes early and not using up precious time, money, and resources on genotypes that will never be released.

### i. PROTEIN ANALYZER

Grain protein content is measured by determining the amount of nitrogen in a wheat sample. It is expressed as a percentage of the sample weight at a standard moisture level. In the USA, protein is expressed as a percentage on a 12.0% moisture content (Carver, 2009). GPC and TWT can be measured by a FOSS Infratec$^{TM}$ 1241 Grain

Analyzer following the AACC Methods 39-00, 39-10, 39-11, and 39-25, and expressed on a 12 percent moisture basis (American Association of Cereal Chemists. Approved Methods, 2000).

## ii. THOUSAND KERNEL WEIGHT

Kernel weight of wheat is measured in commercial sectors as the weight of 1,000 kernels (TKW) measured in grams (Carver, 2009). It is generally counted by electronic seed counters.

## iii. MILLING

The milling properties of wheat are fundamental to many uses of wheat. Millers have a large control over the flours they produce. They can also control the mill specifications such as wheat blends, mill flow, roll speed, sieve sizes and various other specifications. This control helps millers produce a consistent flour with consistent quality. Unfortunately, small-scale test mills do not have the same amount of flexibility, but this allows differentiation between the samples when it comes to measuring the separation of the wheat endosperm, germ, and bran (Carver, 2009). Small-scale milling equipment such as the Brabender Quadrumat Jr. mill, allows the estimation of flour extraction, yield, ash and particle size (Peña et al., 2008). Small-scale milling can be accomplished through the experimental milling AACC approved method 26-10A (American Association of Cereal Chemists. Approved Methods, 2000). For hard wheats such as HRSW, flour extraction is one of the more important parameters obtained from milling.

## iv. NIRS

Near-infrared spectroscopy (NIRS) may be used for the analysis of protein, moisture, ash, and kernel hardness. It has the ability to measure flour or whole grain and provides a versatile and fast estimate of many parameters (Peña et al., 2008). NIR is an accurate method for GPC and FPC. It is based on the correlation of sample spectra and a standard reference. It is conducted using the AACC approved methods 39-00, 39-10, 39-11, and 39-25 (Carver, 2009) (American Association of Cereal Chemists. Approved Methods, 2000). The NIR is a reliable, cheap, and precise instrument in determining protein content and therefore, has been a cornerstone in many breeding programs.

## v. MIXOGRAPH

The mixograph was developed by the National Manufacturing Company in Lincoln Nebraska as a means of studying the action of high-speed commercial mixers in the USA. It is used by following the AACC Method 54-40A, (American Association of Cereal Chemists. Approved Methods, 2000). The mixograph is a recording dough mixer (RDM) that is a staple of wheat science. Dough requires known and repeatable processing that is best achieved by RDMs. The curves created by an RDMs can be partitioned into two portions. One is a rising portion of the curve prior to peak where the flour is hydrating, and dough development is occurring. And the second part is the descending portion where the dough breaks down as a result of continued and then overmixing. The differences in mixing times and time to the peak development are indicative of differences in mixing times of commercial products. Faster time to peak development can be indicative of weaker dough strength and can be associated with

lower mixing tolerances. In the descending portion of the curve, rapid reduction in resistance to mixing, steep angles and faster decreases in the bandwidth of the mixing curve can also be associated to lower mixing tolerance and weak dough strength. (Carver, 2009). The mixograph offers versatility because it allows the evaluation of smaller quantities of flour as compared to the Farinograph, extensograph, and alveograph. The mixograph parameters mixing time and tolerance are highly correlated to the strength and extensibility parameters from the alveograph or extensograph (Peña et al., 2008). In figure 1.2, some of the major parameters that the mixograph measures is the time to peak, also known as the maximum mixing resistance for both mid-line (MP) and top of envelope (TP), the percent of full scale (value, %). The time to peak and peak heights are generally the most meaningful measurements of the mixograph. A mid-line peak time of 3 to 5 minutes and about 60% of scale are the best values for bread-making. Also, steep left-of-peak and right-of-peak slopes are undesirable for both mid-line (ML and MR) and top of envelope (TL and TR). They can indicate a flour sample with low tolerance and a high sensitivity to mixing time. The sum of the absolute values for the sum of left-of-peak and right-of-peak slopes for both the envelope and mid-line analyses can be a single value for the measure of mixing stability and tolerance. A small value indicates a flat, stable, curve. A large value indicates a rapid rise and breakdown which is generally undesirable (Walker, 2004).

### vi. GLUTOMATIC

The Glutomatic measures a number of variables that include wet gluten content, dry gluten content, and the gluten index. It is used by following the AACC Method, 38.12.02

(U.S. Wheat Associates, 2017) (American Association of Cereal Chemists. Approved Methods, 2000). The above method is based on the Glutomatic Gluten Washer and Gluten Index centrifuge and measures both quantity and quality of wet gluten. According to the Glutomatic Systems Operation Manual by Perten Instruments, Gluten is separated from flour by the Glutomatic by being centrifuged to force wet gluten through a specially constructed sieve. The sieve allows for the collection of both the part of the gluten that remains on the sieve and the part that passes through it. The total weight of the gluten is the gluten quantity and the percentage of wet gluten remaining on the sieve after centrifugation is defined as the Gluten Index (GI). If the gluten is very weak all of the gluten may pass through the sieve and the gluten index is 0. If nothing passes through the sieve, the Index is 100. Wet gluten content (WGC) is measured by washing flour with a saltwater solution to remove starch from the sample. The gluten content is expressed on a 14% moisture basis. It is used to estimate the gluten quality or strength by subjecting the wet gluten material through a mesh in a centrifuge. The percentage remaining is called the gluten index (GI) and is an indication of gluten strength (Perten Instruments, 2008). Wet gluten is highly correlated with the protein content in wheat (Carver, 2009).

## B. GENOTYPE X ENVIRONMENT INTERACTION

When genotypes are tested in different environments, it is observed that the rank or performance of the genotype varies depending on the environment. This is called the genotype-by-environment interaction (GE). The need for growing different cultivars in different locations is due to the GE interaction (Yan et al., 2000). GE interaction is one of the major challenges for plant breeders. In Peña (2008), the interaction variance for

FPC for 30 genotypes in 17 locations was smaller than the variance for genotype. This can indicate a particular genotype can have the potential to produce a specified end-use quality (Peña et al., 2008). In Khazratkulova et. Al (2015), they found significant GE interactions in 30 genotypes for yield, TKW, TWT, GPC, and Gluten traits. Peña (2008) also described previous studies that showed mixograph and baking parameters had a larger variation for environment than genotype, but their GE interaction variance was smaller than genotype by itself. This would indicate that the environment would play a big role in the outcome of those traits, but since the genotype variance is larger than the GE interaction variance, the rank of the genotypes for these traits would still be the same from different environments. The genotype ranking for these traits differed depending on the environment which demonstrates a complex effect of environments on said traits. Many traits are quantitatively inherited and require appropriate genetic analysis in order to select and breed for their improvement. Most quantitative traits are controlled by many minor genes where their expression is dependent on the environment. In order to detect GE interaction affects you would normally need to test genotypes in several environments within replicated trails. When a large number of genotypes are tested in several environments, resources may limit data collection, and may lead to non-replicated trials. This can lead to problems when trying to analyze trials in different years and locations. It is difficult to analyze GE interactions in non-replicated trials. There are various methods in order to help breeders account for this GE interaction and overcome unbalanced, incomplete, or non-replicated data sets (Wu et al., 2012). Two of the most popular methods include mixed linear models and biplot analysis.

## C. LINEAR MIXED MODEL ANALYSIS

Linear mixed model (LMM) analysis can be used for variance component estimation. There are three common approaches which include maximum likelihood (ML), restricted maximum likelihood (REML), and minimum norm quadratic unbiased estimation (MINQUE). ML and REML require normally distributed data and involve intensive iteration. However, MINQUE does not require normally distributed data nor iteration. This allows for faster computation and application to more forms of data. In Wu (2012), the equations and process for LMM analysis is explained. First, you use the general genotype-by-genotype x environment (GGE) model, where environment is a combination of location and year, as shown in equation 1:

$$y_{ijkr} = \mu + G_i + E_j + (GE)_{ij} + \epsilon_{ijr} \qquad \text{Eq. 1}$$

Where $y_{ijk}$ is the observed value for replicate $r = 1\ to\ n_r$ , genotype $i = 1\ to\ n_g$, environment $j = 1\ to\ n_l$; $\mu$ is the grand mean; $G_i$ is the main effect of genotype $i = 1\ to\ n_g$; $E_j$ is the main effect of environment $j = 1\ to\ n_l$; $(GE)_{ij}$ is the interaction effect between genotype $i$ and environment $j$ ; $\epsilon_{ijk}$ is the random error for replication $r$ genotype $i$ at environment $j$. Secondly, in order to examine location and year separately, this model can be extended to a genotype-location-year (GLY) model as shown in equation 2:

$$y_{ijkr} = \mu + G_i + L_j + Y_k + (GL)_{ij} + (GY)_{ik} + (LY)_{jk} + (GLY)_{ijk} + \epsilon_{ijkr} \qquad \text{Eq. 2}$$

Where $y_{ijk}$ is the observed value for replicate $r = 1\ to\ n_r$ , genotype $i = 1\ to\ n_g$, location $j = 1\ to\ n_l$, and year $k = 1\ to\ n_y$; $\mu$ is the grand mean; $G_i$ is the main effect of genotype $i = 1\ to\ n_g$; $L_j$ is the main effect of location $j = 1\ to\ n_l$; $Y_k$ is the main effect of year $k = 1\ to\ n_y$; $(GL)_{ij}$ is the interaction effect between genotype $i$ and location $j$ ; $(GY)_{ik}$ is the interaction effect between genotype $i$ and year $k$; $(LY)_{jk}$ is the interaction effect between location $j$ and year $k$; $(GLY)_{ijk}$ is the three-way interaction effect between genotype $i$, location $j$, and year $k$; $\epsilon_{ijk}$ is the random error for replication $r$ genotype $i$ at location $j$ in year $k$. But in order to use MINQUE the above equation is expressed in the forms of vectors and matrices as shown in equation 3:

$$y = 1\mu + U_G e_G + U_G e_G + U_L e_L + U_Y e_Y + U_{GL} e_{GL} + U_{GY} e_{GY} + U_{LY} e_{LY} + U_{GLY} e_{GLY} + e_e$$

$$y = Xb + \sum_{u=1}^{8} U_u e_u \qquad \text{Eq. 3}$$

Where y is an observation vector with dimension n x 1, known; 1 is the vector with all elements 1; $\mu$ is the population mean, unknown; $e_G$ is the random genotype effect vector, $e_G \sim (0, \sigma_G^2 I)$; $U_G$ is the incidence matrix for genotype effects; $e_L$ is the random location effect vector, $e_L \sim (0, \sigma_L^2 I)$; $U_L$ is the incidence matrix for location effects; $e_Y$ is the random year effect vector, $e_Y \sim (0, \sigma_Y^2 I)$; $U_Y$ is the incidence matrix for year effects; $e_{GL}$ is the random GL effect vector, $e_{GL} \sim (0, \sigma_{GL}^2 I)$; $U_{GL}$ is the incidence matrix for GL effects; $e_{GY}$ is the random GY effect vector, $e_{GY} \sim (0, \sigma_{GY}^2 I)$; $U_{GY}$ is the incidence matrix for GY effects; $e_{LY}$ is the random LY effect vector, $e_{LY} \sim (0, \sigma_{LY}^2 I)$; $U_{LY}$ is the incidence matrix for LY effects; $e_{GLY}$ is the random GLY effect vector, $e_{GLY} \sim (0, \sigma_{GLY}^2 I)$; $U_{GLY}$ is the incidence matrix for GLY effects; $e_e$ is the vector for random errors, $e_e \sim (0, \sigma_e^2 I)$.

In Wu (2012) variance components are estimated by MINQUE normal equation for u, v=1,..,8 in equation 4 and 5:

$$[tr(U_u^T Q_\alpha U_v^T U_v Q_\alpha U_u)][\alpha_u^2] = [y^T Q_\alpha U_u U_u^T U_v Q_\alpha y] \quad \text{Eq. 4}$$

Where, the trace tr is the sum of diagonals of a matrix, and

$$Q_\alpha = V_\alpha^{-1} - V_\alpha^{-1} X (X^T V_\alpha^{-1} X)^{-1} X^T V_\alpha^{-1} \quad \text{Eq. 5}$$

Where, $V_\alpha = \sum_{u=1}^{r} \alpha_u U_u U_u^T$, and $V_\alpha^{-1}$ is the inverse matrix of $V_\alpha$ with prior values $\alpha_u$ in place of $\sigma_u^2$ in $V_\alpha$ (Wu et al., 2012).

The end result of LMM analysis and objective is estimating the variance components. Proportional variance components can also be calculated by taking the ratio for each Variance component by the phenotypic variance. The phenotypic variance ($V_p$) was defined as $V_p = V_G + V_{GL} + V_{GY} + V_{GLY} + V_e$ where, $V_G = \sigma_G^2$ for genotypic effects; $V_{GL} = \sigma_{GL}^2$ for GL effects; $V_{GY} = \sigma_{GY}^2$ for GY effects; $V_{GLY} = \sigma_{GLY}^2$ for GLY effects. The ratio of $V_G/V_P$ is considered the heritability of the genotype. The ratio $V_G/(V_{GL} + V_{GY} + V_{GLY})$ can also be useful in comparing the genotype effect to the GE interaction effect (Wu, 2003). The proportional variance components are extremely useful in determining the proportion of variance that is due to the variance component for each trait. This is the objective of most GE LMM analysis. These results can show how much proportion each effect in the GGE model contributes to the trait. Genetic, location, and year effects can also be estimated by adjusted unbiased prediction approach (AUP) which can help determine the individual effects for each genotype, location, and year from the population mean. In addition to MINQUE component estimation, the GGE model can also use

Jackknife resampling approach to calculate standard error for each component along with calculating the strength of the estimates by conducting a simulation study for the genetic model evaluation. This can calculate estimates, standard errors, and testing powers. (Rasul et al., 2015).

## D. BIPLOT ANALYSIS

Biplot analysis was developed in 1971 and has become a common method in variety trial data analysis. Biplot analysis is a visualization tool that can graphically address many research questions. Biplot analysis and statistical analyses are joined for the analysis of data for a single trait to address: spatial and field analysis from a single trait, mega-environment analysis from multiple years, location evaluation based on data from multiple years, and genotype evaluation based on data from multiple years. Genotype evaluation and decision-making based on multiple traits, the analysis in studying trait associations in different environments, and the study of location-by-trait (LT) patterns can also be analyzed by biplot analysis (Yan, 2014).

### i. THEORETICAL BASIS

The main objective for most plant breeders is genetic gain. In Yan (2013), genetic gain is composed of three factors in the equation, $\Delta G = ih^2\sigma_p$, where $\Delta G$ is genetic gain, $i$ is the selection intensity, $h^2$is the heritability, and $\sigma_p$ is the square root of the phenotypic variance, $\sigma_p^2$.

# 1. HERITABILITY

Heritability is the ratio of the genotypic variance, $\sigma_g^2$, over the phenotypic variance. Heritability is the single most important factor in quantitative genetics due to the fact that selection intensity is an arbitrary value dependent on the breeding program and the genotypic variance is constant for a set of genotypes. Most measurements in variety trials and statistical analysis is to improve heritability.

Heritability also is estimated in genotype-location-year (GLY) research and models. The linear model for this combination is the genotype-by genotype x environment interaction (GGE) model shown previously in equation 1. The variance components for this model are used to calculate the phenotypic variance and is shown in equation 6:

$$\sigma_p^2 = \sigma_g^2 + \frac{\sigma_l^2}{n_l} + \frac{\sigma_y^2}{n_y} + \frac{\sigma_{gl}^2}{n_l} + \frac{\sigma_{gy}^2}{n_y} + \frac{\sigma_{ly}^2}{n_l n_y} + \frac{\sigma_{gly}^2}{n_l n_y} + \frac{\sigma_\epsilon^2}{n_l n_y n_r} \quad \text{Eq. 6}$$

Where $\sigma_p^2$ is the phenotypic variance; $\sigma_g^2$ is the genotypic variance; $\sigma_l^2$is the location variance; $\sigma_y^2$ is the year variance; $\sigma_{gl}^2$ is the genotype-by-location (GL) interaction variance; $\sigma_{gy}^2$ is the genotype-by-year (GY) variance; $\sigma_{ly}^2$ is the location-by-year (LY) variance; $\sigma_{gly}^2$ is the genotype-by-location-by-year variance, $\sigma_\epsilon^2$ is the experimental error variance, $n_l$ is the number of locations, $n_y$ is the number of years, and $n_r$ is the number of replications . To compare genotypes, their effects for year, location, and location-year are the same and therefore, $(\sigma_l^2, \sigma_y^2, \sigma_{ly}^2)$ are all zero and can be removed from the above equation making the phenotypic variance as shown in equation 7:

$$\sigma_p^2 = \sigma_g^2 + \frac{\sigma_{gl}^2}{n_l} + \frac{\sigma_{gy}^2}{n_y} + \frac{\sigma_{gly}^2}{n_l n_y} + \frac{\sigma_\epsilon^2}{n_l n_y n_r} \quad \text{Eq. 7}$$

Using the above variance components, the heritability for the genotype-location-year model can be shown in equation 8:

$$H_{lyr} = \frac{\sigma_g^2}{\sigma_p^2} = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gl}^2}{n_l} + \frac{\sigma_{gy}^2}{n_y} + \frac{\sigma_{gly}^2}{n_l n_y} + \frac{\sigma_\epsilon^2}{n_l n_y n_r}} \quad \text{Eq. 8}$$

Where heritability *H* ranges from 0 to 1 with 1 meaning that all of the observed differences between genotypic effects are completely due to genetic differences.

## 2. SVD AND PC ANALYSIS

Yan (2013) explains how singular value decomposition (SVD) is the backbone of the biplot. It separates a matrix P of m rows and n columns (m x n) into three matrices G, L, and E as shown in equation 9.

$$P_{mxn} = G_{mxk} L_{kxk} E_{nXk}^T \quad \text{Eq. 9}$$

G is a matrix of (m x k), L is a non-negative diagonal matrix (k x k), and $E^T$ which is the transpose of E and is a matrix (n x k), with k=min(m,n). The k columns of G and the K columns of E are called left-singular vectors and right-singular vectors of P. The diagonal entries of L are known as the singular values of P. This is why the process is called singular value decomposition. SVD can also be the process to decompose matrix P into k principal components (PC), with each containing a vector of row scores $(\xi)_i$ a vector of

column scores $(\eta)_j$, and a singular value $(\lambda)$, and each element in P can be recovered by equation 10:

$$p_{ij} = \sum_{l=1}^{k} \xi_{il}\lambda_l\eta_{lj} \quad \text{Eq. 10}$$

Where $\lambda_l$ is the singular value for the lth PC; $\lambda_l^2$ is the eigenvalue of P for the lth PC, which equals to the sum of squares (SS) of matrix P explained by the lth PC; $\xi_{il}$ is the score for row I on the lth PC; and $\eta_{lj}$ is the score for column j on the lth PC. The implementation of SVD involves complex iterations. The results of subjecting matrix P to SVD and results in three matrices, the vector of singular values, the row matrix characterizing the row factors, and the column matrix characterizing the column factors. This also creates three PCs, and each PC has three parts which are a singular value, a row vector, and a column factor. The number of PCs required to approximate matrix P need to fully explain the variation of the matrix and is expressed a $k \leq \min(m, n)$, where k is called the rank of the matrix. However, in order to construct a biplot, $p_{ij}$ from above has to be rewritten as shown in equation 11:

$$P_{ij} = \left(\xi_{i1}\lambda_1^f\right)\left(\lambda_1^{1-f}\eta_{j1}\right) + \left(\xi_{i2}\lambda_2^f\right)\left(\lambda_2^{1-f}\eta_{j2}\right) + \epsilon_{ij} \quad \text{Eq. 11}$$

The singular values are partitioned into the row and column vectors such that matrix P is decomposed into two matrices rather than three. This allows the matrix P to be expressed as the product of the row vector and the column vector. The matrix P can then be displayed as a biplot. $f$ is a factor called the singular value partitioning factor. It can have a value between 0 and 1. There are three ways to focus the biplot using $f$. If $f$=1 it is a row-focused singular value partition. If $f$=0, it is a column-focused singular value

partition, and if $f$=0.5, it is a symmetrical singular value partition. The last one is called symmetrical partition; it is preferred when the interactions between the rows and columns are of interest. This is used for additive main effect and multiplicative interaction (AMMI) analysis. Applying the above methods to the PCs from subjecting SVD to matrix P results in PC scores for each row and column. These are the scores used to construct a biplot (Yan, 2014).

## ii. INCOMPLETE DATA

Biplot analysis has limitations similar to other analysis procedures. Its use of singular value decomposition (SVD) is a major limitation when it comes to unbalanced data, because SVD requires a complete two-way table. Breeders find it hard to have balanced multi-year data due to the introduction and removal of various experimental cultivars in their data sets. This is because inferior genotypes are usually dropped, and new genotypes are added yearly. Many research objectives require multi-year data, and therefore, unbalanced data or incomplete data becomes a significant limitation in analysis. There are various ways to analyze an imbalanced data set. This includes: extracting a balanced data set by removing missing values, filling in the missing values with environmental means, and filling in the missing values with estimated values from various methods.

In Yan (2013), the proposed procedure for the estimation of the missing values in a two way table, where a multiyear data set of year-location-genotype trait dataset is converted into a two-way table where the environment is year-location, is where the missing cells are first filled in with 0 and then subjected to SVD analysis and the missing

values are predicted from the results of the first two principal components (PC). The predicted values fill in the missing values and then SVD estimation is performed again. This is repeated in iteration until the predicted values are similar to the iteration previous. This difference is measure as $d = [(1/n)\sum_{i=1}^{n}(x_i - x_i')^2]^{1/2}$, where d is the difference between predicted values in the current iteration, $x_i$ is the predicted value for the ith missing value in the current iteration, $x_i'$ is that in the previous iteration, and n is the total number of missing values. The grand mean from the two-way table was calculated as $\bar{y} = \left[(1/N)\sum_{i=1}^{m}\sum_{j=1}^{n} y_{ij}^2\right]^{1/2}$, where $y_{ij}$ is the value in the ith row and jth column that is not a missing value and N is the total number of valid values. This value was used to remove the sign, negative or positive, to give weight to large absolute values. The iteration process is done when the values in two successive iterations are similar enough which is generally defined as $d/\bar{y} < 0.01$. In Yan (2013) the conclusion was that the prediction worked well with large datasets that had up to 60% of the data as missing. The successful use of the procedure requires the data to be big enough where a valid pattern is derived, because the prediction process uses and generates missing values on the existing pattern in the data. Yan (2013) suggest that the estimation procedure to be used when the missing values are less than 40% to allow smaller data sets to be used. However, the process works well when there is a strong association between environments. The stronger correlation between environments, the more reliable the prediction process becomes. If an environment is completely independent of all other environments, then the procedure may not provide meaningful predictions for the environment in question (Yan, 2013).

## iii. SINGLE-YEAR DATA ANALYSIS

Single-year data analysis is the analysis of multilocation trials in a single year. It can be from a three-way dataset of genotype-location-trait. The three-way data can be reorganized into two-way table that can analyze genotype-by-location for a single trait, genotype-by-trait for each location, all locations, or a selection of locations. Another application is a location-by-trait tale for each genotype, all genotypes, or a group of genotypes. For most data analysis, the genotype-by-location for a trait is the most useful for identifying and evaluation traits and genotype-by-trait is very important if the objective to evaluation and identify superior lines and cultivars (Yan, 2014).

### 1. GENOTYPE-BY-LOCATION ANALYSIS

The goal of genotype-by-location (GL) analysis is to evaluate superior lines in regard to certain key traits. Since genotype evaluation is dependent on the environment. The key outcomes of GL analysis are to understand the environment, locations. And eliminate inferior genotypes. Single-year analysis is primarily used for preliminary analysis. GL can also be used to reveal human errors if the trait analyzed is highly heritable. Since traits that are highly heritable are rather constant and less variable between environments, any differentiation in results can be surmised by human error. GGE biplot can facilitate the visualization of the genetic correlations between locations in ranking the genotypes based on the trait in question. The angles between locations are an indication of the magnitude of G vs GE. A strong negative correlation can indicate different mega-environments. Genotype evaluation may be analyzed in GL analysis and can be used to identify widely or specifically adapted genotypes. For widely adapted

genotypes, comparing the Mean vs. Instability for of the biplot which includes all locations can be used. This can be done using the average environment and an average environment axis (AEA) and coordination (AEC) on the biplot. AEA is a single-arrowed line in a biplot that passes through an origin, which is a grand mean of effects. The arrow points to a higher genotypic effect or value. The AEC is a double arrowed line that passes through the origin perpendicular to the AEA. The arrows point towards higher instability. The further a genotype is from the AEC, the more unstable it is and the bigger GE interaction. The further away from the origin on the AEA a genotype is, the further it gets from the grand mean. This can be interpreted as more or less compared to the mean depending on which side of the origin it is on, with a bigger effect the closer to the arrow a genotype is. Ideal genotypes should have the highest possible mean and stability. The ideal genotype location on the axis is generally shown with a small circle and is located on the AEA showing no instability. Location evaluation to identify suitable locations for genotype evaluation can also be done through GL analysis. Locations with low heritability can mask genetic differences. Heritability can be estimated with a GL biplot with h-weighted data. The vector length of a location estimates its h and the cosine of the angle between locations estimates the genetic correlation between them (Yan, 2014).

## 2. GENOTYPE-BY-TRAIT ANALYSIS

Genotype-by-trait (GT) analysis is similar to GGE biplots except that instead of location or environment, trait is used, and the data is scaled with the unit removed. Scaling is done using the standard deviation. GT analysis is used to understand the relations among traits and understand how traits fluctuate within a genotype. The

interpretation of a GT biplot is very similar to a GGE biplot. The cosine of the angle between two traits estimates the correlation between them. A short vector length of a trait in the biplot generally is an indication that the trait has a weak association with all other traits. Due to strong GE interactions, associations among traits may differ quite a lot depending on the location. If the biplot does not account for most of the variation, then the correlations may not be accurate. GT analysis can reveal important relations among key traits and can be used to create breeding goals and selection strategies for a trait. Negative correlations among traits can make breeding for certain traits challenging. Therefore, GT analysis can be used for multi-trait selection. Multi-trait selection can be completed by independent selection, independent culling, and index selection. Independent selection is selecting a genotype based on a single trait, this is used for selecting parents for a new cross. This is done quite a bit for specific adaption and end-use traits. Independent culling is discarding genotypes if it does not meet breeding objectives even if other traits are good. This is used for selection superior lines because superior lines are selected based on its biggest limiting factor. Index selection is selection based on an index based on breeding objectives. Index selection is mainly done in conjunction with one of the other selection methods (Yan, 2014).

## 3. LOCATION-BY-TRAIT ANALYSIS

Another major purpose for variety trails and breeding is to select location suitable for trait and genotype analysis. Location-by-trait (LT) or environment-by-trait (ET) analysis can be used to identify locations that are suitable for producing specific end-use quality traits. LT is very similar to GT, except that genotype is location. It's interpretation

is very similar I that the cosine of the angle between two traits estimates the location correlation (Yan, 2014).

## iv. MULTI-YEAR DATA ANALYSIS

Multi-year variety trial data is a year-location-genotype trait four-way table that can be converted into various two-way tables with the most common way of having the environment being the combination of year and location. Multi-year data analysis has three objectives when it comes to genotype-by-environment and are similar to the single-year genotype-by-location objectives. The objectives are mega-environment analysis, test location evaluation, and genotype evaluation. Multi-year analysis can be used to show the repeatability across years of trials and various evaluations. The biggest challenge to multi-year analysis is incomplete and unbalanced data sets, but the problem has been addressed above by Yan (2013) as the development of SVD to estimate or predict the missing values. Mega-environment analysis, location and genotype evaluation is then conducted using the completed data set (Yan, 2014). Generally, there are three ways to analyze multi-year data, the first being to analyze yearly and summarize across years, and the second is to average the multi-year data into a genotype-by-location table and conduct GGL (genotype by genotype-location) biplot analysis. The first option is very common and are only good indicators when the yearly patterns are strongly correlated. However, the second option does take into account genotype-by-year or genotype-by-location-by-year interactions. The third option is to conduct PC analysis for each year and location and then PC analysis for each location average among years. However, this option allows PC scores to represent the same location and patterns and can obscure the real pattern.

That is why GGL + GGE, which is a genotype-by-location biplot with the genotype-by-environment (location + year), biplot is the best approach. It allows the visualization of G vs. GE, GL vs GE, or GY and GLY (Yan, 2015). In Yan (2015), explains that mega-environment and location evaluation are given increasingly more attention because they are prerequisites for effective genotype evaluation. Mega-environment and location analysis needs to be based on multiple years because the environments in a single year is only a sample of the environment of a whole (Yan, 2015).

## 1. MEGA-ENVIRONMENT EVALUATION

Yan (2015) explains a mega-environment as an area of a crop's growing region that is fairly homogenous and produces similar results. Differentiation happens when genotypes perform differently in subregions across multiple years. Because of this, genotype evaluation is based on mean performance, and selection based on mean performance may not be the correct method due to genotypes that are best in all mega-environments but may not be the best in any of them. The main purpose of analysis is to optimize a variety evaluations and recommendation for certain areas. To properly analyze a mega-environment, there are three steps. First, you generate a GGE biplot to display the genotype-by-environment with each location represented by multiple points. Next, you generate a GGL + GGE biplot. Locations are then defined as a single point based on the mean coordinates of the specific location. The last step is once a pattern is identified in the GGL + GGE biplot, a GGS + GGE biplot is created to display the mega-environment classification, with a mega-environment defined as a single point with the mean

coordinates of all location-year combinations within the subregions. GGS is a genotype-by-subregion interaction (Yan, 2015).

## 2. LOCATION EVALUATION

Location evaluation is very important in genotype evaluation, because the evaluations are only relevant if the locations represent your mega-environment of interest. The two aspects of evaluation of a location is choosing the best location and choosing multiple locations dependent on your objective. A location needs to be representative of a mega-environment in most years. Multiple locations should provide a good range of representation of the mega-environment or region. Location evaluation is based on a GGL + GGE biplot within each mega-environment. The cosine of the angle between a location and the (AEA) or the projection of a test location onto the average environment axis of the mega-environment, which is a measure of the representativeness of the location for the mega-environment, with the longer being the better. The longer a projection the more representative of the environment in most years. A shorter projection means the location is more variable among years. Locations with a longer projection are better locations for multi-year trails due to the smaller variation (Yan, 2015).

## 3. GENOTYPE EVALUATION

Genotype evaluation is generally the ultimate goal for most breeders and variety trials. This is the basis of most cultivar recommendations. Mega-environment and location evaluation need to be understood before meaningful genotype evaluation can be done. Genotype evaluation based on multi-year analysis allows for genotypes to be

compared even if they were not grown in the same year, because of this ability, genotype evaluation may be predictive in multi-year analysis. If genotype evaluation is done in just a single year, you may only be able to discard inferior genotypes and not properly evaluate the superior ones. Superior genotypes need to have both high mean performance and high stability across environments. Genotype evaluation to discard inferior genotypes may be accomplish in a variety of ways. You can discard all genotypes lower than the poorest check in mean performance. You can discard all genotypes lower than the poorest check based on mean performance and stability. You can discard all genotypes whose mean performance is significantly lower than the best genotype, and finally discard all genotypes whose mean performance is significantly lower than the best check. Biplots can rank genotypes based on mean and stability very similar to GL genotypes from single-year analysis. Genotype stability may also be evaluated in biplot analysis. Stability may be measured in various ways such as rank indices, additive main effect and multiplicative interaction (AMMI), and regression methods. It is a measure of the heritability across locations and years (Yan, 2014).

# IV. OBJECTIVES

Hard Red Spring Wheat (*Triticum aestivum* L.) is characterized by generally high protein content and excellent baking and milling performance. The ability for millers, bakers, and other end-users of wheat to properly and cheaply produce food products with uniformity is dependent on the consistency of the quality characteristics. To enable producers and breeders to grow the highest and most consistent quality wheat, they must choose varieties best-suited to local environments. Therefore, in order to assist breeders,

agronomists, and growers, the objective of this experiment was to determine how production year and locations influenced end-use quality traits.

Chapter 2 focused on a broad overview of HRSW grown throughout South Dakota. It analyzed the various traits and variables from common screening methods used by breeders for their ability to run a high-rate of small samples through them, which include a protein analyzer, thousand kernel weight, mill, NIR, mixograph, and glutomatic. The averages and trends for each variable from the above tests for the varieties, counties, and years represented in the study was summarized into a quality report that can be informative to growers, breeders, and millers alike, and represents a large-scale study of HRSW in South Dakota. The objective was to show trends of how production year and locations influenced end-use quality traits and will identify trends to compliment statistical analysis to achieve the main objective of determining how production years and locations influenced end-use quality traits.

Chapter 3 focused on the GGE and biplot analysis to predict and estimate how varieties, locations, and years influenced HRSW grown in South Dakota and provide statistical analyses for the trends in chapter 2. Chapter 3 focused heavily on statistical analysis to identify the best locations and varieties for each trait. This information may be helpful in identifying the interactions of genotypes and environments to explain stability of varieties and traits in various counties throughout South Dakota and support the hypotheses in chapter 2 and determine how production years and locations influenced end-use quality traits.

This study will assist breeders, agronomists, and growers, in understanding which varieties are least susceptible to quality fluctuations, and therefore, most desirable to end-users. It may help breeders in selecting varieties to cross with, and to select environments to test for specific traits. It will enable growers to identify the best varieties for their locations and will show millers and buyers the best locations and varieties to purchase from in the hope to increase value and production of HRSW grown in South Dakota.

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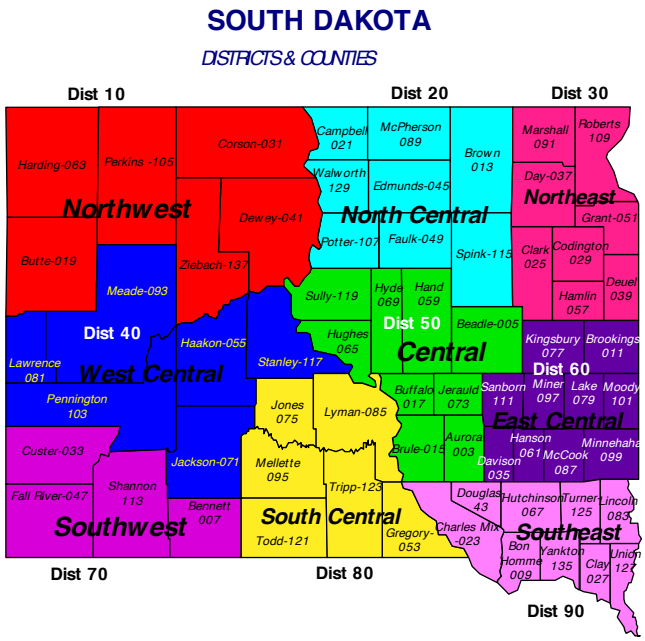


Figure 1.1. USDA, South Dakota Crop Reporting Districts

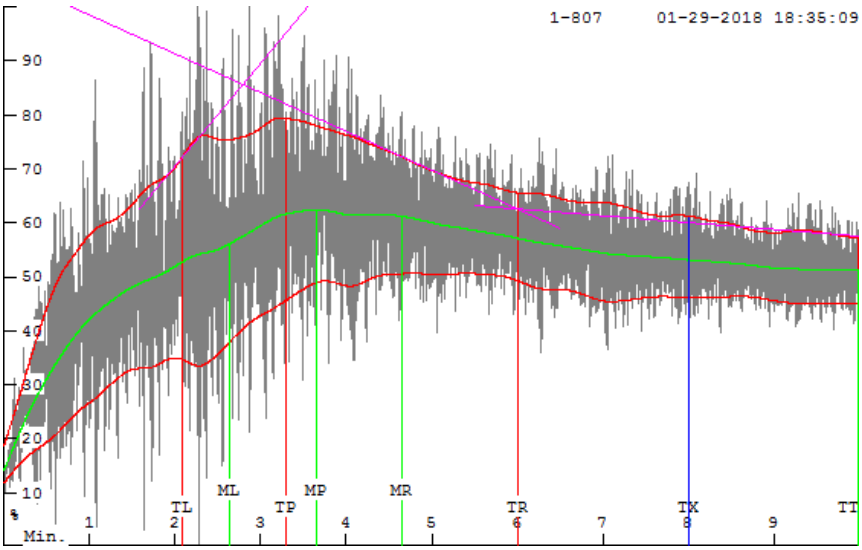


Figure 1.2. Common Mixograph parameters. TL: top-of-envelope left-peak; ML: mid-line left-of-peak; TP: top-of-envelope peak; MP: mid-line peak; MR: mid-line right-of-peak; TR: top-of-envelope right-of-peak.

Table 1.1. USDA Crop Reporting Districts, Spring Wheat Production in South Dakota

| Ag District | ACRES HARVESTED | ACRES PLANTED | PRODUCTION, BU | YIELD, BU / ACRE |
|---|---|---|---|---|
| CENTRAL | 188,500 | 237,500 | 6,972,000 | 37 |
| EAST CENTRAL | 11,100 | 11,200 | 576,000 | 51.9 |
| NORTH CENTRAL | 319,000 | 326,500 | 14,336,000 | 44.9 |
| NORTHEAST | 119,000 | 122,000 | 6,326,000 | 53.2 |
| NORTHWEST | 185,000 | 199,000 | 7,023,000 | 38 |
| OTHER DISTRICTS[a] | 85,900 | 92,400 | 3,146,000 | 36.6 |
| SOUTH CENTRAL | 48,900 | 53,000 | 1,890,000 | 38.7 |
| SOUTHWEST | 7,600 | 8,400 | 261,000 | 34.3 |
| SOUTH DAKOTA[b] | 965,000 | 1,050,000 | 40,530,000 | 42 |

[a]OTHER DISTRICTS: Combination of West Central and South East

[b]Total production for entire state of South Dakota

# CHAPTER 2: QUALITY REPORT OF HARD RED SPRING WHEAT IN SOUTH DAKOTA

## ABSTRACT

Hard Red Spring Wheat (HRSW; *Triticum aestivum* L.) is characterized by generally high protein content and excellent baking and milling performance. The ability for millers, bakers, and other end-users to properly and cheaply produce food products with uniformity is dependent on the quality consistency of wheat produced by breeders and farmers.

To determine which variety to grow in certain locations, more data has to be collected in order to evaluate how end-use quality fluctuates in specific locations. The objective was to identify trends and locations to compliment statistical analysis to achieve the main objective of determining how production years and locations influenced end-use quality traits.

One thousand four hundred and twenty-three HRSW samples from seven years and thirty-eight counties throughout South Dakota comprised of twelve varieties were evaluated for twenty-one traits and variables from common screening methods. The averages and trends for each trait for the varieties, counties, and years were reported.

Summary statistics reveal that Steele-ND and Traverse were the best and worst performing varieties, respectively, 2010 and 2015 were the best and worst years, and finally, districts and counties in the North West and North East were the best and worst locations, respectively, in regard to end-use quality traits.

This is supported by the noticeable trend that as grain protein increases, so do various gluten index parameters and mixograph mixing times and values. This signifies a need for further statistical comparison to support the observed results.

# INTRODUCTION

Hard Red Spring Wheat (HRSW; *Triticum aestivum* L.) is characterized by generally high protein content and excellent baking and milling performance. The ability for millers, bakers, and other end-users of wheat to properly and cheaply produce food products with uniformity is dependent on the consistency of the quality of wheat produced. Therefore, the ability for breeders and farmers to grow consistent high end-use quality spring wheat is very important. Wheat is graded into five grades, numbered one through five. Grading factors such as test weight, characterize wheat in relation to milling quality but do not grade the quality or end-use performance of flour. Quality is considered a non-grade factor but influences the value and outcomes for buyers and millers. Common non-grade quality factors can include moisture, protein, ash content, enzyme activity, as well as dough and baking characteristics. Millers and bakers place great emphasis on non-grade factors even though they are not included in the Federal Grain Inspection Service (FGIS) grading system (Carver, 2009).

Kernel quality, also known as grain quality, has many grade and non-grade factors. All of the grade factors discussed previously are based on kernel quality. However, when it comes to quality, non-grade factors are the best indicators of wheat end-use quality and bread-making potential. Test weight, thousand kernel weight, and most importantly, protein content are very important traits that can be measured without the need for milling flour or baking bread.

Flour quality is the conformance to various measurable characteristics that are significant in terms of end use. Flour quality is the ability of the flour to produce a

uniform, good end-use product defined by suppliers and buyers. Flour strength is tantamount to quality due to the strength of the flour and dictates the sustainability of the flour for specific end uses. There are many methods that evaluate flour strength that measure characteristics of the flour (Pomeranz & Hlynka, 1971). Flour quality can be measured by various tests that measure rheological and physical characteristics of the flour. Physical properties of doughs from different wheats are of major concern to bakers. Consistent dough properties are necessary for quality control of baked goods. Broad ranges in dough development, strength, elasticity, and extensibility are needed in baking for the various end-use products. (Pomeranz & Hlynka, 1971).

Bread-making potential and quality is the culmination of all the quality traits and testing. Bread is the most common end-use product of HRS wheat, and all the quality tests attempt to measure important factors of wheat in its ability to make consistent bread. None of the tests can fully predict bread-making quality and performance of flour on their own. They serve as indexes that correlate to the final end-use product and can help predict the performance of flour. The baking test is the final and ultimate test of flour quality. However, they require a large volume of grain, baking facilities and are subjective in nature requiring well trained staff, making baking tests expensive. This process makes it difficult for a high-throughput screening method. Thus, the use of other various high-throughput testing methods that can test small samples in a short period of time for certain quality traits and parameters and can be used to measure grain and flour quality and help predict bread-making potential (Pomeranz & Hlynka, 1971).

Along with higher yield, improved quality is a primary objective of most wheat breeders. However, due to a negative correlation between high yield and high protein,

breeders find it difficult to obtain both (Khazratkulova et al., 2015). Since protein is strongly associated with bread-making quality, breeders need to give protein and grain quality the same level of importance as yield and disease resistance. In order to develop cultivars, breeders need to understand the genetic control of quality traits, the relationship between quality traits and processing qualities, and achieve high-throughput rapid identification of quality traits by using quick, reliable, low-cost methodologies.

There are various tests used to measure quality, but the important ones used by plant breeders are high-throughput and help measure quality and the overall bread-making quality of the kernels and flour of wheat. The complex and additive nature of inheritance of most quality traits has led to the development of a range of indirect tests (Peña et al., 2008). These tests can be applied at all levels of the breeding process, and their ability to measure small samples allows for evaluation in early generations. This can make breeding programs more efficient by allowing breeders to discard inferior genotypes early and avoid investing resources in genotypes that will never be released.

In 2018, HRS wheat was planted on 1,050,000 acres and 965,000 acres were harvested in South Dakota at an average of 42 bushels/acre according to the USDA National Agricultural Statistics Service (NASS) (www.nass.usda.gov). The top producing crop reporting district in 2018 was North Central with 326,500 acres planted and 319,000 acres harvested with an average yield of 44.9 bushels/acre. The next highest producing districts had over 100,000 less acres showing there is massive potential for the increase in acreage and production for spring wheat within the spring wheat producing areas of South Dakota. Each year a U.S Hard Red Spring wheat regional quality report is produced by US Wheat Associates. However, these do not look at the local level. In

South Dakota, there is typically a wide range of climate and weather conditions from county to county. To properly determine which variety to grow in certain locations, more data should be collected in order to evaluate how it fits into specific locations and more importantly, whether its quality levels are prone to large fluctuations or remain quite consistent.

This study presents a broad overview of HRS wheat grown throughout South Dakota and the analysis of the various traits and variables from common screening methods used by breeders for their ability to analyze a large number of small samples, which include a protein analyzer, thousand kernel weight, mill, NIR, mixograph, and glutomatic. The averages and trends for each trait for varieties, counties, and years represented is summarized into a report that is similar to that of the annual report procuded by US Wheat Associates. This report should be very informative for growers, breeders, and millers alike, and represents a large-scale study of HRS in South Dakota. Exploratory analysis was then done on the dataset to understand the unbalanced dataset and allow proper analysis. The objective was to identify trends and locations to compliment statistical analysis to achieve the main objective of determining how production years and locations influenced end-use quality traits.

# MATERIALS AND METHODS

One thousand four hundred and twenty-three HRSW samples were collected from the Seed Testing Laboratory at South Dakota State University. These samples represented certified seed samples from twelve varieties, seven years and thirty-eight counties throughout South Dakota. Variety, county, and year were the three main factors for consideration, but counties were also further grouped into districts categorized by the USDA to help compare with production results presented in Table 2.1. The USDA crop reporting districts in South Dakota represented in this study are Central, East Central, North Central, North East, North West, South Central, South East, and West Central (Figure 2.1). The counties represented in this study for the Central district are Beadle, Hand, Hyde, Jerauld, and Sully. The district East Central is represented by Brookings, Hanson, Hughes, Kingsbury, Lake, Minnehaha, Moody, and Sanborn counties. The district North Central is represented by Brown, Campbell, Edmunds, Faulk, McPherson, Potter, Spink, and Walworth counties. The district North East is represented by Clark, Codington, Day, Deuel, Grant, Hamlin, Marshall, and Roberts counties. The district North West is represented by Corson and Dewey counties. The district South Central is represented by Jones, Lyman, and Tripp counties. The district South East is represented by Charles Mix, Douglas, and Hutchinson counties. West central district is only represented by one county and that is Pennington.

Six varieties included in this study were developed in South Dakota while the remaining six were from North Dakota or Minnesota. Varieties analyzed were ‘Advance’, ‘Barlow’, ‘Brick’, ‘Briggs’, ‘Faller’, ‘Forefront’, ‘Howard’, ‘Prosper’, ‘RB07’, ‘Select’,

‘Steele-ND’, and ‘Traverse’. Since the evaluated samples were from certified seed samples submitted to the Seed Testing Laboratory, they were a random collection, though dependent on those available for production at that time of submission. The data set was unbalanced and not all varieties were grown in each county or year. All varieties were represented by at least 40 samples with a few having almost 300 samples. Also, the number of samples per county and year were random and unbalanced with certain counties that produce more wheat on average, having more samples represented in the study.

All samples were evaluated for twenty-one quality traits. These parameters were divided into three categories, kernel, flour, and dough quality traits. Three kernel quality, parameters were measured; test weight (TWT), thousand kernel weight (TKW), and grain protein content (GPC). Flour traits measured were flour extraction (EXT), ash content (ASH), flour protein content (FPC), gluten index (GI), wet gluten content (WGC), dry gluten content (DGC), and water-binding (WB). The dough quality traits measured were water absorption (ABS), top-of-envelope variables, peak time (EPT), peak value (EPV), left-of-peak slope (ELS), right-of-peak slope (ERS), mixing stability (MSE), and mid-lines variables peak time (MPT), peak value (MPV), left-of-peak slope (MLS), right-of-peak slope (MRS), mixing stability (MSM). Quality test analysis procedures were performed as described by (Caffe-Treml et al., 2010).

Grain samples were analyzed for TWT and GPC based on a 12% moisture basis, using a FOSS Infratec$^{TM}$ 1241 Grain Analyzer following AACC methods 39.10 and 39.11. Grain protein content is expressed in percentage and TWT is expressed as

kilogram/hectare (kg/hl). Thousand kernel weights were also taken by measuring the weight of 1,000 kernels and reported in grams.

Grain samples were then tempered to 15% moisture with distilled water to obtain a total weight of 70 grams following the AACC method 26-95 (American Association of Cereal Chemists. Approved Methods, 2000). After conditioning for at least 16 hours, samples were milled in a Quadrumat Jr. mill (C.W. Brabender Instruments, South Hackensack, NJ). Milled samples were then put in a rotating US #60 sieve (250-µm aperture) to separate the bran from the flour. Separated flour was then weighed to determine EXT, based on a total weight of 70 grams, (grams of flour)/(70 grams)*100, and expressed as a percentage.

Flour samples were analyzed with a Foss NIR System Model 6500 Monochromators (Foss, Laurel, MD) for ASH and FPC, on a 14% moisture basis following the AACC approved method 39-11 (American Association of Cereal Chemists. Approved Methods, 2000). Flour samples were also analyzed for gluten quality. As described in (Lu, 2017), the Gluten Index method is used to measure quality of wheat flour. Gluten index is determined by the Glutomatic system (Perten Instruments, AB, Sweden) and is a measure of gluten strength regardless of the quantity of gluten present. The Glutomatic measures a number of variables that include WGC, DGC, WB, and GI. The steps in detail, for the Gluten index method, follows the AACC Method, 38.12.02 (American Association of Cereal Chemists. Approved Methods, 2000). First, 10.0 g ± 0.01 g of wheat flour is weighed and put into the Glutomatic wash chamber with an 88 micron polyester sieve. Then 4.8 ml of salt solution (2% sodium chloride solution) is

added to the flour samples. Next, the flour and salt solution are mixed to form a dough during the first 20 seconds then after the end of the mixing phase, the washing automatically starts and continues for five minutes with a liquid flow rate of 50- 56 ml/min. Thirty seconds after completed washing, the wet gluten piece is transferred to the special sieve cassette and centrifuged for one minute at 6000 ± 5 rpm in the Centrifuge 2015. Next, the fraction that passed through the sieves is scraped off with a spatula and weighed. The fraction remaining on the inside of the sieve is collected and added to a balance, and the total wet gluten weight is obtained. Next, the total wet gluten piece is dried at 150 °C during four minutes in the Glutork 2020. When dry, the gluten is weighed on a balance. Finally, the calculations are done. The centrifugal force causes some of the wet gluten to pass through the sieve. The amount of gluten remaining on the inside of the sieve after centrifuging in relation to total wet gluten weight is denoted as the Gluten Index (GI). Wet gluten content is expressed as the total wet gluten weight ((g)/10 (g) *100). Dry gluten content is obtained by drying the wet gluten in the Glutork 2020 gluten dryer. Dry gluten content is expressed as (dry gluten weight (g)/10 (g) *100). Water binding in wet gluten is defined as the difference between wet gluten content and dry gluten content. Gluten content is expressed on a 14% moisture basis. It is used to estimate the gluten quality or strength by subjecting the wet gluten material through a mesh in a centrifuge. The percentage remaining is called the gluten index (GI) and is an indication of gluten strength (Perten Instruments, 2008). Wet gluten is highly correlated with the protein content in wheat (Carver, 2009).

As described in (Caffe-Treml et al., 2010), a mixograph (National Mfg. Co., Lincoln, NE USA) fitted with a 10-g bowl was used to measure dough rheological

properties. Mixing speed was 88 rpm and test duration was 10 min. Water amounts added to each flour sample was determined based on the water absorption estimates obtained with NIR spectroscopy. Water absorption (ABS) estimates were based on protein estimates from the NIR as described in AACC method 54-40A. Mixograph parameters were obtained and recorded with Mixsmart software (v.3.8). There are numerous parameters recorded by the Mixsmart software, but the parameters analyzed in this study were dependent on the instructions for interpreting a mixograph report in the Mixsmart software user manual. The major parameters that the mixograph measures is the time to peak, also known as the maximum mixing resistance for both mid-line (MP) and top of envelope (TP), the percent of full scale (value, %). The sum of the absolute values for the sum of left-of-peak and right-of-peak slopes for both the envelope and mid-line analyses .can be a single value for the measure of mixing stability and tolerance. A small value indicates a flat, stable, curve. A large value indicates a rapid rise and breakdown which is generally undesirable (Walker, 2004). Mixsmart software for top-of-envelope parameters are EPT, EPV, ELS, ERS, and MSE and mid-line parameters are MPT, MPV, MLS, MRS, and MSM were reported.

Averages and standard deviations for all quality traits and parameters were calculated for each variety, county, district and year using the R statistical analysis packages (“base” and “stats”) (R Core Team, 2018), and graphs to display trends were created in Microsoft Excel, version 16.21.1. Exploratory Analysis was then conducted on the dataset using R version 3.5.1 and JMP Version 14.0. Histograms and Q-Q lines were created for each trait using R package “base”. Shapiro-Wilk test for normally distributed data was completed using JMP for all traits individually and all traits for each factor.Then

the sample size, range, kurtosis and skewness for each factor and trait combination were completed using JMP. Finally, boxplots were created for each factor and trait using the R package “ggplot2” (R Core Team, 2018).

# RESULTS AND DISCUSSION

## Summary Statistics

### Kernel Quality

The three kernel quality traits measured were GPC, TKW, and TWT. Average GPC for all samples was 14.35% and the standard deviation was 1.19. Average TKW for all samples was 29.84 grams, and the standard deviation was 4.29. Likewise, the average TWT for all samples was 81.57 kg/hl, and the standard deviation was 2.84.

Averages and standard deviations for each variety are presented in Table 2.2. The variety, Barlow, had the highest average GPC at 15.03 % as well as one of the lowest standard deviations, showing a more consistent higher value. Traverse had the lowest average GPC at 13.43% and slightly lower standard deviation than the average. Howard had the highest TKW at 32.96 grams and Select had the lowest average TKW at 27.87 grams. Traverse also had the lowest TWT on average at 78.31 kg/hl and Brick had the largest TWT at 83.12 kg/hl. Most of the varieties had very similar standard deviation for GPC and TWT compared to the average standard deviation.

Averages and standard deviations of these three traits for each county are presented in Table 2.3. According to this table, Moody county had the largest GPC, which averaged 16.40%, but this is only based on one sample and therefore had no standard deviation and Minnehaha had the lowest GPC on average at 12.2% and also was only based on a single sample. Therefore, for counties with more than one sample, Hutchinson and Grant counties had the highest and lowest average GPC at 15.23% and

13.50%, respectively. Hughes county had the lowest TKW on average at 26.09 grams and Grant county had the highest TKW on average at 35.16 grams. Hanson county had the lowest TWT on average at 77.45 kg/hl and Hamlin county had the highest TWT on average at 83.57 kg/hl.

Table 2.4 shows averages and standard deviations for the above 3 traits for USDA districts which are provided in figure 2.1. The district with the highest average GPC was the North West district at 14.76% while the East Central district had the lowest average GPC at 14.02%. The South Central district had the lowest TKW at 27.43 grams and the North East District had the highest TKW at 31.09 grams. The South East district had the lowest average TWT at 79.76 kg/hl and the West Central district had the highest TWT on average at 82.26 kg/hl.

Table 2.5 contains averages and standard deviations of kernel quality traits for the 7 years represented. Table 2.5 reveals that GPC was lowest in 2015 with an average of 13.49% and GPC was highest in 2011 which averaged 14.90%. However, 2011 had the lowest average TKW of 25.67 grams and 2010 had the highest that was 32.96 grams. The highest TWT was noted in 2015 at 83.19 kg/hl and the lowest was 2011 with an average of 80.27 kg/hl.

Kernel quality traits are the most important end-use traits for producers because they are measures that correlate with higher production and quality of grain which help to determine the value of their crop. Therefore, the higher the values the better. TWT is a factor in wheat grading. There was no variety, county, district, or year where the average TWT values were below the minimum level of 76.4 kg/hl for U.S. Grade 1 HRS wheat,

and therefore, all were sufficient in regard to TWT. Also, according to (U.S. Wheat Associates, 2017), U.S. market HRS wheat prices are quoted for 14% GPC and premiums and discounts are specified for percentage points above or below that level. There were three varieties with averages below this 14% threshold; Advance, Howard, and Traverse. There were also only a few counties with average GPC below the threshold and no district average below 14%. 2015 was the only year in which average GPC was below the threshold. The years 2011 and 2012 were above average for GPC. From the summary statistics there does not appear to be a strong trend between the traits, where Traverse had the lowest GPC and the lowest TKW, while for years, 2015 had the lowest GPC, but the highest TWT. Overall, South Dakota wheat was above the 14% GPC threshold with TWTs that were well above the minimum level, and a TKW close to 30 grams.

**Flour Quality**

The seven flour quality traits measured were EXT, ASH, FPC, GI, WGC, DGC, and WB. Average EXT for all samples was 58.81% and the standard deviation was 3.02. Average ASH for all samples was 0.30% and the standard deviation was 0.04. Average FPC for all samples was 14.21% and the standard deviation was 1.16, which is slightly lower than GPC. GI average for all samples was 90.02 and the standard deviation was 10.45. Averages for the remaining gluten traits, WGC, DGC, and WB, are 36.17%, 12.92%, and 23.25%, respectively. Standard deviation for these traits are 4.14, 1.46, and 2.85, respectively.

Averages and standard deviations for each variety are shown in Table 2.6. Table 2.6 reveals that Select had the lowest EXT with an average of 56.01% while Howard had

the highest average EXT with 61.59%. The variety ASH averages all had very small standard deviations and Forefront had the lowest average ASH content with 0.25% while Select had the highest average ASH content with 0.34%. Flour protein content values were similar to GPC values and again, Traverse had the lowest average FPC with 13.28%, but Steele-ND had the highest average FPC at 14.94%. The change of the highest average variety between GPC and FPC may be due to EXT values. Traverse also had the lowest average GI at 71.30, which reveals a weak gluten and low protein trend for this variety. Advance had the highest average GI with a high value of 97.64. In contrast to GI, Advance had the lowest average WGC with 32.58% while Steele-ND had the highest average WGC with 38.41%. Forefront had the lowest average DGC with 11.80% while Steele-ND had the highest average DGC with 13.66%. Advance had the lowest average WB with 20.77 while Steele-ND had the highest average WB with 24.75. Advance had contrasting gluten quality vs quantity values, with a high GI, indicating high gluten quality, but low content values.

Table 2.7 contains the averages and standard deviations for flour quality traits for each county. Focusing on counties with more than one sample, Pennington county had the lowest average EXT at 55.83% while Beadle county had the highest average EXT at 61.57%. Grant county had the lowest average ASH at 0.26% while Hutchinson county had the highest average ASH at 0.35%. Grant county had the lowest average FPC, WGC and DGC with 13.26%, 33.31% and 11.83%, respectively. Hughes county had the highest average FPC at 15.01%. Faulk county had the highest average WGC at 39.06%. and Corson county had the highest average DGC at 13.493%. For the remaining gluten traits, Hanson county had the lowest average GI at 75.28 while Hughes county had the highest

average GI at 95.38. Jerauld county had the lowest average WB at 21.42 while Faulk county had the highest average WB at 25.16. These results reveal that Grant county generally had the lowest protein and gluten content related values.

Averages and standard deviations for flour quality traits in each district are contained in Table 2.8. Table 2.8 reveals that the West Central district had the lowest average EXT at 55.83% while the East Central district had the highest average Ext at 59.38%. The South Central district had the highest average ASH content at 0.33%. The East Central district had the lowest average FPC at 13.88% while the North West district had the highest average FPC at 14.66% but had the highest average WGC and DGC at 38.09% and 13.69%, respectively. The North East district had the lowest ASH, WGC, DGC, and WB with 0.28%, 35.33%, 12.64%, and 24.47, respectively However, similar to our earlier results, the North East district actually had the highest average GI at 91.82.The South East district had the lowest average GI at 78.77, and the highest average WB at 24.47.

Table 2.9 contains the averages and standard deviations for flour quality traits for each year. Table 2.9 revealed that 2011 had the lowest average EXT at 56.79%. However, 2011 had the highest average FPC at 14.56%. 2008 had the highest average EXT at 61.05%, and the lowest average ASH content at 0.27%. 2013 had the highest average ASH content at 0.31%. 2015 had the lowest average FPC at 13.24%. 2010 had the lowest average GI at 85.56 and 2015 had the highest average GI at 95.01. In similar contrast, 2015 had the lowest gluten content values but the highest GI, and 2010 had the opposite trend. The WGC, DGC, and WB for 2015 were 32.30%, 11.46%, and 20.84%,

respectively. 2010 had the highest values for WGC, DGC, and WB with 37.52%, 13.30%, and 24.23%, respectively.

Desirable flour quality traits are high EXT and FPC because the flour extraction is important for milling profitability, while FPC is just as important as GPC, because protein is the single largest indicator of bread-making ability and performance of end-use quality. Higher values for gluten traits GI, WGC, DGC, and WB, indicate high-end use quality and measure the gluten quantities and bread strength in samples. If the gluten is weak all of the gluten may pass through the sieve and the gluten index is 0. If nothing passes through the sieve, the Index is 100. Therefore, a higher GI indicates a strong gluten and better bread structure. Summary statistics reveal that Steele-ND, Howard, and Briggs have the largest flour extraction values. Steele-ND also had the largest FPC, WGC, DGC, and WB values. For South Dakota varieties, Briggs, which had one of the highest EXT values, also is one of the top varieties FPC, WPC, DGC, and WB. As expected from the trends of the kernel quality results, 2015 had the lowest FPC, WGC, DGC, and WB while interestingly enough having the largest GI average. Trends of high GI values with low FPC and other gluten traits are reflected in both counties and districts, where for example, the North East district had the highest GI but lowest WGC, DGC, WB and the second lowest FPC value. South Dakota wheat had an average GI of 90, FPC above 14%, and a WG of 36.17%.

**Dough Quality**

Eleven dough quality traits were measured. These traits were ABS, EPT, EPV, ELS, ERS, MSE, MPT, MPV, MLS, MRS, and MSM. Top-of-envelope and mid-line

parameters are two different methods to measure the mixograph curve and present similar results. Average MPT for all samples was 4.36 minutes and the standard deviation was 1.22. Average MPV for all samples was 55.71% and the standard deviation was 4.11. Averages for the slope variables MLS and MRS for all samples were 5.77% and -1.99%, respectively. Standard deviations were 3.22 and 1.50 for MLS and MRS. Average MSM for all samples was 7.82% and the standard deviation was 3.94. Averages and standard deviations for the top-of-envelope parameters are similar to the mid-line values and are contained in Tables 2.10 through 2.17.

Averages and standard deviations for each variety are contained in Table 2.10 and 2.11. Varieties with the lowest and highest average ABS were Traverse and Steele-ND with 63.52% and 66.01%, respectively. Traverse had the lowest average values for MPT, and MRS, and the highest average values for MLS and MSM. Average values of Traverse for MPT, MRS, MLS, and MSM were 3.24 minutes, 7.01%, -3.85%, and 10.93%, respectively. This confirms the previous results that Traverse had poor overall end-use quality. Brick had the highest average MPT at 5.73 minutes. Prosper had the lowest average MPV at 52.45% while Steele-ND had the highest average MPV at 58.76%. Select had the lowest average MLS at 4.36 while Faller had the highest average MRS at -1.18%. Select had the lowest average MSM at 5.87% Averages and standard deviations for the top-of-envelope parameters are similar to the mid-line values and are contained in Tables 2.10 through 2.11.

Tables 2.12 and 2.13 provide averages and standard deviations for dough quality traits for each county. These tables reveal that for counties with more than one sample, Grant county had the lowest average ABS  63.49% while Hughes county had the highest

average of 66.10%. Jerauld county had the lowest MPV, MLS and MSM on average with 52.49%, 3.07%, and 4.60, respectively. Hutchinson county had the highest MLS and MSM on average and the lowest MRS on average at 59.90%, 12.27, and -3.34%, respectively. Hanson county had the lowest average MPT at 2.75 minutes while Hyde county had the highest average MPT at 5.20 minutes. Finally, Hamlin county had the highest average MRS at -1.26%. Averages and standard deviations for the top-of-envelope parameters are similar to the mid-line values and are contained in Tables 2.12 through 2.13.

Tables 2.14 and 2.15 contain the averages and standard deviations for dough quality traits for each district. These tables reveal that the North West district and North East districts had similar trends seen in varieties and years for other quality traits, The North West district had the highest ABS, MVP and lowest MLS and MSM on average with 65.60%, 56.24%, 4.78%, and 6.94%, respectively. The North East district had the highest MPT and MRS on average with 4.49 minutes and -1.79%, respectively. The East Central district had the lowest average ABS at 64.41% and the highest MLS and MSM on average with 6.58% and 9.28%, respectively. The South East district had the lowest average MPT and MRS at 3.56 minutes and -3.17%, respectively. The Central district had the lowest average MPV at 54.97%. Averages and standard deviations for the top-of-envelope parameters are similar to the mid-line values and are contained in Tables 2.14 through 2.15.

Averages and standard deviations for dough quality traits for each year are contained in tables 2.16 and 2.17. Tables 2.16 and 2.17 reveal that 2015 had the lowest average ABS at 63.45% while 2011 had the highest average ABS at 65.44%. 2010 had

the lowest MPT on average of 3.56 minutes while 2013 had the highest average MPT at 5.07 minutes. The lowest and highest MPV averages were from 2015 and 2010 with 52.38% and 57.95%, respectively. 2013 had the lowest MLS at 4.61% and 2010 had the highest MLS at 7.32% on average. 2010 had the lowest average MRS at -2.83% and 2012 had the highest average MRS at -1.39%. 2013 had the lowest average MSM at 6.20% and 2010 had the highest average MSM at 10.20%. Averages and standard deviations for the top-of-envelope parameters are similar to the mid-line values and are contained in Tables 2.16 through 2.17.

Higher dough quality trait values are not necessarily the best or most desired. According to the mixograph handbook, (Walker, 2004), the time to peak and peak height values are generally the most meaningful measurements of the mixograph. A MPT of 3 to 5 minutes and an MPV of 60% of scale are the best values for bread-making. Also, steep left-of-peak and right-of-peak slopes are undesirable for both mid-line and top of envelope. They can indicate a flour sample with low tolerance and a high sensitivity to mixing time. Most varieties meet the MPT range and all of them are below the MPV 60% value. The varieties that fit these requirements the best are Barlow, Howard, and Steele-ND, because they have the closest MPV value to 60%. However, in comparing these varieties to other dough quality traits such as MSM, they do not necessarily have the lowest most stable values. Select was the variety with the lowest average MSM, which indicates a stable flat curve but Select had a lower than average MPV value. Following the above criteria, Hyde had the highest MPV value awhile staying in between the MPT range of 3 to 5 minutes, but just like the varieties, had one of the largest MSM values. Jerauld county had the lowest MSM, but a relatively small MPV. This continuing

trend shows that it may be difficult to find a location and variety that meets all the requirements. Summary statistics reveal that most years fall within the desired MPT range with 2010 having the highest MPV value, and similar to varieties and locations, had the highest MSM value. Overall, the average dough quality results show that the MPT falls within the desired range but had a low MPV value.

## Quality Trends

### Variety

While the main objective of this study was to determine how production years and locations influenced end-use quality traits, due to GE interactions, it is also important to determine variety trends. The trend for variety kernel quality was that GPC was positively correlated with TWT. A similar trend was noted for averages of flour quality traits. Specifically, higher FPC resulted in higher GI, WGC, DGC, and WB, with Steele-ND, Barlow, and Briggs having the highest protein and protein related traits. However, Howard which had the highest TKW and TWT was one of only three varieties below the 14% GPC threshold. Among the higher protein varieties, it was noted that dough quality traits such as ABS, EPV, and MPV were also high. Overall, Steele-ND had the best performing end-use quality traits, while Traverse was the worst. Variety trends for all quality traits are presented in figure 2.2, Compared to the Yearly trends in the same figure, they appear to be less consistent between varieties which may signify a larger GE interaction and allow for differentiation and rankings between varieties.

**Years**

Yearly trends appeared to have the opposite trend as variety where the years with high GPC generally had lower TWT and TKW. However, the same trend as the varieties where the high protein years also resulted in higher gluten related traits, MPV and EPV, but lower MPT and EPT. Some of the higher end-use quality traits were produced in 2010 and 2011 while 2015 resulted in overall lower end-use quality. Figure 2.2 contains yearly trends for all quality traits and reveals that averages for most traits in 2011 were lower in other years for kernel quality traits.

**County and District**

County and district trends are similar to both variety and yearly trends in regards that locations with higher protein, generally had the higher protein related traits such as GPC, FPC, WGC, DGC, GI, WB, ABS, and MPV and MPT. This is supported by the observations between the North West and North East districts, in which according to table 2.1, the North West generally had some of the lowest production areas and the North East had some of the higher production areas in South Dakota. Therefore, since protein content is negatively correlated with yield, the North East district had lower protein and protein related traits, whereas the North West had higher average protein and related traits. These trends signify a need for further analysis and correlation between traits.

Trends for how county and years influence each quality trait is shown in figures 2.3 through 2.13. Some years have larger variability between counties than others. For example, in figure 2.3, GPC looks overall very similar, but the counties vary greatly for

2008, which is reflected in it having the highest standard deviation but a close to average value. According to the figures, some traits appear to be more consistent for counties and years. The kernel quality traits, TWT and TKW, appear to have less consistent trends compared to GPC which is supported by the larger average standard deviation. Flour quality traits that appear more consistent between counties are WGC, DGC, and WB, with GI appearing to be more variable especially in the earlier years of 2008 and 2009. The more consistent dough quality traits in the figures are ABS, EPV, ERS, MPV, and MRS again with 2008 being the more variable year between counties for these traits. 2010 and 2008 were more variable than other years for the remaining traits. This trend in years is supported by the fact that 2008 had the largest standard deviation for the majority of traits.

## Exploratory Analysis

### Trait Distribution

The distribution for each individual trait was visually assessed in figures 2.14-2.34 using histograms and quantile plots. Most traits appear normally distributed according to their respective plots. For kernel quality traits, GPC and TKW appear to be normally distributed with TWT skewed at both tail locations. For flour quality traits, ASH appears to have a normally distributed histogram, but the quantile reveals the data is not completely continuous. According to the histogram and quantile plots, GI appears to be not normally distributed, with the histogram skewed to the right. FPC, EXT, WGC, DGC, and WB all appear to have normal distributions according to histograms and quantile plots. For dough quality traits, ELS and MLS have similar distributions and do not appear to be normally

distributed with the data to be skewed to the left. EPT, MPT, EPV, and MPV all appear to be normally distributed while ERS and MRS appear to be skewed to the right. MSE and MSM both appear to be skewed to the left. To confirm the histogram and quantile plots, the Shapiro-Wilk test for normal distribution was completed for all traits and is contained in table 2.18. According to table 2.18, all traits except for EXT, WB, and MPV are statistically significant with p-values under 0.05 and can conclude that for most traits, it is highly unlikely they follow a normal distribution.

**Variety Distribution**

Table 2.19 contains the data distribution statistics for variety kernel quality traits. This table includes the numer of samples (N), the range of values, and the skewness and kurtosis values for each variety. Skewness and kurtosis values are used together to asses the normality of the distribution of data. When used in conjuction with histograms, quantile plots, and shapiro-wilk tests, skewness and kurtosis have excellent abilities to detect departures from normal distributions. Skewness and kurtosis measure the shape of the distribution. Skewness measures symmetry with values close to zero indicating normally distributed data. Kurtosis is the measure of the combined size of tails. Kurtosis for a normal distribution is three, and therefore kurtosis is also reported as the difference from 3, and therefore kurtosis from a normal distribution can be considered 0. If the kurtosis is positive, the tails are larger, and if it is negative, the tails of the distribution are smaller as compared to normally distributed data (Decarlo, 1997).

Overall, there is a different number of samples for each variety with certain varieties have more samples such as Briggs and Brick. Prosper has the smallest number of

samples with 38. The ranges for GPC for most varieties are within 1 or 2% of each other. The range for TWT and TKW are differ more between varieties with Select and Faller having larger ranges. The skewnwss and kurtosis for GPC are all relatively close to zero with Steele-ND having the largest skewness value of 0.71 and Advance having the largest Kurtosis value of 1.38. TWT and TKW have similar results for skewness and kurtosis, except for Steele-ND and Brick have larger kurtosis values. Table 2.19 can be complimented with table 2.43 which contains the shapiro-Wilk test values and significance of a p-value of 0.05 is denoted with and asterisk. For GPC, all varieties except for Brick and Briggs are not significant indicating a large probability for normally distributed data. Thousand kernel weight and TWT has opposite results with most of the varieties having significant values indicating a large probability for not having normally distributed data.

The data distribution distribution statistics for variety flour quality traits are contained in tables 2.23 and 2.27. For EXT, Advance, Howard, and Prosper indicate larger values for skewness and kurtosis. Ash content and FPC has smaller values for skewness and kurtosis for all varieties, indicating more symmetrically shaped data distributions. Gluten index has much larger skewness and kurtosis values which confirm the distribution shape of the overall gluten index data distribution. The kurtosis values for Advance and Brick are extremely large with values of 21.89 and 21.68, respectively. Wet gluten content, DGC, and WB have similar results to FPC and GPC with more symmetrically shaped distributions. The shapiro-Wilk values contained in table 2.44 confirm the results for the distribution of flour quality traits for each variety. Flour protein content, WGC, DGC, and WBC only had a few significant values indicating non-normaly distributed data, whereas ASH and GI values are significant for most of the varieties.

Tables 2.31, 2.35 and 2.39 contain all the variety dough quality distribution statistics. According to table 2.31 and 2.35, there are no varieties with skewness kurtosis above 1 for ABS. For EPT, Briggs and Traverse are the only varieties with larger skewness and kurtosis with values of skewness of 1.22 and 1.50, respectively and kurtosis values of 2.12 and 2.61, respectively. There were no large values for EPV for skewness and kurtosis. Most of the varieties for ELS, ERS and MSE had skewness values between -1 to 1. Mid-line variables had very similar results to top-of-envelope variables. The shapiro-Wilk test values in table 2.45 confirm the results in the previous tables. The results confirm that Briggs is one of the few varieties that is significant for the shapiro Wilk test for most traits, concluding it does not follow normal distribution. For certain traits such as ELS, ERS, MSE, and MSM, most varieties do not follow a normal distribution.

**County Distribution**

The county distribution statistics for kernel, flour, and dough quality traits are contained in tables 2.20, 2.24, 2.28, 2.32, 2.36, and 2.40. The number of samples for each county varies greatly, counties such as Douglas, Minnehaha, Moody, and Sanborn had one sample, while other counties such as Day county, has 226. The skewness and kurtosis values need at least two samples, and therefore there is no values for the counties with only one sample. For the remaining counties, the results are similar to varieties, for flour quality traits such as GPC, TWT, and TKW, most counties had skewness and kurtosis values between -1 and 1. Hughes county had the highest skewness and kurtosis values for GPC at 2.07 and 4.68, respectively. Roberts county had the highest skewness and kurtois values for TWT at -2.15 and 4.92, respectively.

The flour quality distribution statistics contained in table 2.24, reveal that most counties have skewness and kurtosis values close to zero for flour quality traits. In table 2.28, the skewness and kurtosis values for GI reveal a less symmetrical shape for most counties, which again confirm the results seen for the overall trait data and varieties for GI. For the distribution of EXT, ASH, FPC, WGC, DGC, and WB, vary with only a few counties that stand out with higher values of kurtosis and skewness. These counties with less symmetrically shaped distribution are Hughes, Pennington, Clark and Beadle.

The dough quality distribution statistics are contained in tables 2.32, 2.36, and 2.40. Overall, the top-of-envlope traits and mid-line traits are very similar. Most of the counties for dough quality traits have skewness and kurtosis values between -1 and 1, with the exception of Beadle, Brookings, Hughes, Roberts and Tripp counties. Tables 2.49, 2.50, and 2.51 contain the shapiro-Wilk test values for normal distribution for each county and trait. For kernel quality traits GPC, TKW, and TWT, there are only a few counties with a significant shapiro-Wilk test value indicating a non-normal distribution. Flour quality traits have similar distributions as compared to kernel quality traits. Most counties are not significant for the shapiro Wilk test except for GI, in which most counties do not have normally distributed data. Dough quality shapiro Wilk test results reveal that Day, Faulk, and Edmunds counties are significant which contradicts the larger skewness and kurtosis values for the previous counties such as Beadle and Tripp. This shows the importance of using a range of statistics to determine the distribution of a data set. Most counties have normally distributed data for dough quality traits, with a higher proportion of counties having non-normally distrubted data for traits such as MSE and ELS.

**District Distribution**

The district distribution statistics for kernel, flour, and dough quality traits are contained in tables 2.21, 2.25, 2.29, 2.33, 2.37, and 2.41. The results in these table are very similar to the previous distribution results. Districts have small kurtosis and skewness values for kernel quality traits. South East and North East districts do have skewness values above 1, which indicate they may not have symmetrically shaped distributions. The flour quality traits for districts in table 2.25 and 2.29 reveal once again that the district distributions are normal for most traits except for GI, with skewness and kurtosis values outside of the range of -1 to 1. The district North West however, does have higher skewness and kurtosis values for DGC with 2.50 and 11.21, respectively. The district distributions for dough quality traits appear normal with the exception of ELS, ERS, MSE in which most counties have skewness and kurtosis values above 1. Similar to previous results, the top-of-envelope traits have similar distributions as compared to mid-line traits. Overall, the distribution statistics are confirmed by the shapiro-Wilk test values in tables 2.52, 2.53, and 2.54. The shapiro-Wilk test values reveal that most districts have normal distributions for kernel quality traits, except for the North East district for GPC, and the East Central and North Central for TKW. All districts have significant shapiro-wilk test values indicating non-normal distributions, which confirm previous results. Ash content and DGC also have also non-normal distributions for most district while most of the district for EXT, FPC, WGC, DGC, and WB have normal distributions according to table 2.53. The distribution results for dough quality traits in table 2.54 confirm the kurtosis and skewness results that ELS, ERS, and MSE for most districts do not have normal distributions due to significant shapiro-Wilk test values.

**Year Distribution**

The year distribution statistics for kernel, flour, and dough quality traits are contained in tables 2.22, 2.26, 2.30, 2.34, 2.38, and 2.42. The kernel quality distribution statistics in table 2.22 reveal that for GPC, 2008 has large skewness and kurtosis values at -1.84 and 4.65, respectively. For TWT, 2010 has the unsymmetrically shaped distributions with skewness and kurtosis values of -1.29 and 2.37, respectively. All years have skewness and kurtosis values within the -1 to 1 range for TKW. The year flour quality distribution tables 2.26 and 2.30, reveal that 2008 has large values for skewness and kurtosis for EXT, FPC, WGC, DGC, and WB. The other years appear to have more symmetrical distributions for flour quality traits due to the small skewness and kurtosis values. All years have skewness and kurtosis values beyond the normal range for GI. The same trends for years appear in tables 2.30, 2.34, and 2.42 with 2008 having large skewness and kurtosis values for most dough quality traits, while the other years have values closer to 0. Similar to the previous results, ELS, ERS, andMSE have larger skewness and kurtosis values with similar results for the mid-line traits. These results are confirmed with the shapiro-Wilk test values in tables 2.46, 2.47, and 2.48. These tables confirm the trends in the distribution statistics with 2008 have significant values for most traits. Only a few years have significant values for GPC indicating non-nomral distributions. Test weight however, has significant values for all years exvept 2008 and 2015 indicating non-normal distributions. All years have significant values for GI and most have significant values for ASH and DGC also. Table 2.48 confirms the trends seen in the distribution statistics with ELS, ERS, and MSE have significant values for almost all years.

The trends seen in the distribution statistics of skewness, kurtosis, and shapiro-Wilk test values indicate that overall, individual traits appear to have less normally distributed data seen in the fact that the distribution statistics indicate non-normal distributions throughout all factors. These traits are GI, ELS, ERS, and MSE, which are also confirmed from the previous histograms and quantile plots. For more explorations in comparing factors, boxplots were analyzed to obtain insight into the different levels of each factor.

**Kernel Quality Boxplots**

The boxplots for year, variety, county, and district factors are contained in figures 2.35, 2.36, and 2.40. Boxplots are created for visual representation of quantiles, outliers, and means and allow visual comparisons between the individual boxplots. The boxplots for GPC in figure 2.35, reveal that districts appear to have less variance between levels than variety, year, and county with county having much larger differences between levels. It is apparent from the boxplots that counties vary greatly in observations and distributions with a larger number of outliers as compared to the other factors. Comparing boxplots for varieties, Barlow and Steele-ND appear to have larger means for GPC which are also indicated by the averages reported previously and are represented as diamonds in the boxplots. The large range and outliers in county boxplots create difficulty when comparing between counties. The boxplots for TWT are contained in figure 2.36. The boxplots reveal similar trends as compared to GPC with similar boxplots for all districts and large contrasts between boxplots for counties. There also appears to be more outliers towards the smaller values of TWT for all factors. The varieties and years with the larger means also support averages in previous tables such as Forefront and Advance. Thousand kernel weight boxplots for each factor are shown in figure 2.37. The boxplots reveal that 2011 has much

lower TKW on average as compared to the other years. Also, another revealing visualization is the large number of outliers towards the higher end of TKW values for Faller.

**Flour Quality Boxplots**

The boxplots for flour quality traits for all factors are represented in figures 2.38 through 2.38, and 2.40 through 2.45. The boxplots for ASH reveal a large amount of variation between varieties compared to the previous flour quality traits. Barlow appears to have most of the quantiles close together as compared to the other varieties with outliers on both tails of the distribution. The higher averaging ASH boxplots appear to be Faller, Prosper, and Select. There also appears to be an increasing trend of ASH from year to year ending in the year 2013. The trends for county are similar to previous traits with large difference between counties. However, there also appear to be differnces between district which contrast flour quality traits. Flour protein content boxplits in figure 2.40 reveal similar boxplots for between years, varieties, and districts. Flour extraction boxplots in figure 2.41 illustrates the differences between factors. There are more obvious differences between levels as compared to GPC. The boxplots show that Howard appear to have the highest EXT which comifrms the averages reported previously. Figure 2.42 contains the boxpltos for GI which immediately reveals the skewed distribution of the GI data. These boxplots reveal the outliers that are responsible for the non-normal distribution revealed in the distribution statistics, histograms and quantile plots. This problem complicates the comparison between levels for each factor and makes it difficult to visualize trends. Wet gluten content, DGC, and WB boxplots in figures 2.43 through 2.25, visualize very similar results. These traits show very similar results between years and districts with varieties

revealing more variance between levels. There is also an apparent trend for these traits that show a decreasing mean as years progress.

**Dough Quality Boxplots**

Figures 2.39, and figures 2.46 through 2.55 contain the boxplots dough quality traits. Figure 2.39 includes the boxplots for ABS. The boxplots for year and districts appear very similar between levels. There does appear to be larger difference between the distributions of the various varieties. The largest mean for ABS for varieties are Steele-ND and Barlow. The boxplots for ELS, ERS, MLS, MRS, MSE, and MSM all appears skewed in distribution with a large number of outliers which makes it difficult to compare levels for each factor. Figure 2.47 illustrates the boxplots for EPT. These boxplots reveal the large difference in means between varieties, with Brick and Advance have the two largest means. District boxplots appear very similar with no discernable difference in distribution except for South East and West Central districts. Also, 2012 and 2013 appear to have the largest EPT means between the years reported. The MPT values are very similar to EPT. The boxplots in figure 2.48 display the distribution and means for EPV. The diffrerence between within districts and years appear relatively small with more variance appearing between the different varieties. Also, the boxplots for counties with enough samples to define a proportional boxplot appear similar. The boxplots for MPV appear very similar and are contained in figure 2.52.

Overall, the exploratory analysis reveals that certain traits such as GI, ELS, ERS, and MSE may need to be transformed or analyzed with appropriate models to accurately predict statistical effects. The differing distributions and sample size for each level of the

reported factors may also affect the outcome for statistical analysis and taken into account in order to avoid violating assumptions. For most traits, district and years appear to have similar distributions and means  while there appears to be larger difference between varieties, which could possibly indicate ability to discriminate between varieties for most traits. However, these boxplots and distribution statistics are purely visual and indications of distribution and require further statistical analysis to confirm the overall trends and effects. The exploratory analysis is an important part of statistical analysis and is vital in understanding the data and what models will produce the most accurate results.

# CONCLUSION

Based on this quality report, trends and summary statistics of end-use quality traits measured by the common screening methods selected for this study, support the idea that quality traits related to bread-making ability increase as protein content increases (U.S. Wheat Associates, 2017). This is supported by the trends noted among all the factors that as protein content increases so does the various gluten index parameters and the mixograph mixing times and values. Trends for districts and counties also support the known negative correlation between protein and yield that is widely known (Khazratkulova et al., 2015). The higher average protein locations also were the lower producing districts according to table 2.1. The trend between all factors signifies a need for further statistical comparison in the form of correlations between all quality traits to support the trends. For other traits such as TKW, TWT, and the other mixograph parameters, no conclusive trend between years, counties, and varieties can be made from the summary statistics. However, some traits appear to be more consistent based on standard deviation and figures than others and need further exploration. The conclusion determined from summary statistics, Steele-ND and Traverse were the best and worst varieties, respectively, in regard to end-use quality traits, 2010 and 2015 were the best and worst years, respectively, in regard to end-use quality traits, and finally, districts and counties in the North West and North East are the best and worst locations, respectively, in regard to end-use quality traits.

It is difficult to properly compare the county and year trends due to not all counties being present in all years. This is also problematic for other factors explored

above. All of these conclusions are based on summary statistics and visual trends in the tables and graphs. However, no conclusive results can be achieved without proper statistical analysis. The trends for overall county and district averages can be perceived, but to be more useful, exploration into individual factors and their interactions should be shown. Thus, there is a need for further statistical analysis to explore the statistical effects and comparison of individual years, counties, and varieties on end-use quality and achieve the objective of determining how production year and location influenced quality traits.

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Table 2.1. USDA Crop Reporting Districts, Spring Wheat Production in South Dakota.

| Ag District | ACRES HARVESTED | ACRES PLANTED | PRODUCTION, BU | YIELD, BU / ACRE |
|---|---|---|---|---|
| CENTRAL | 188,500 | 237,500 | 6,972,000 | 37 |
| EAST CENTRAL | 11,100 | 11,200 | 576,000 | 51.9 |
| NORTH CENTRAL | 319,000 | 326,500 | 14,336,000 | 44.9 |
| NORTHEAST | 119,000 | 122,000 | 6,326,000 | 53.2 |
| NORTHWEST | 185,000 | 199,000 | 7,023,000 | 38 |
| OTHER DISTRICTS[a] | 85,900 | 92,400 | 3,146,000 | 36.6 |
| SOUTH CENTRAL | 48,900 | 53,000 | 1,890,000 | 38.7 |
| SOUTHWEST | 7,600 | 8,400 | 261,000 | 34.3 |
| SOUTH DAKOTA[b] | 965,000 | 1,050,000 | 40,530,000 | 42 |

[a]OTHER DISTRICTS: Combination of West Central and South East
[b]Total production for entire state of South Dakota

Table 2.2. Variety Kernel Quality Trait Averages and Standard Deviations over Analysis Years and Production Environments.

| | | GPC[a] (12% moisture basis) | | TWT (kg/hl) | | TKW (grams) | |
|---|---|---|---|---|---|---|---|
| Variety | N[b] | Average | SD[c] | Average | SD | Average | SD |
| ADVANCE | 68 | 13.98 | 1.01 | 82.81 | 2.06 | 29.13 | 3.40 |
| BARLOW | 89 | 15.03 | 0.99 | 82.77 | 2.08 | 28.42 | 3.24 |
| BRICK | 209 | 14.40 | 1.08 | 83.12 | 2.39 | 28.64 | 4.07 |
| BRIGGS | 287 | 14.51 | 1.16 | 81.70 | 2.32 | 32.17 | 3.65 |
| FALLER | 106 | 14.15 | 0.99 | 80.05 | 2.44 | 30.55 | 5.07 |
| FOREFRONT | 44 | 14.00 | 1.20 | 82.99 | 2.53 | 28.98 | 2.97 |
| HOWARD | 43 | 13.82 | 1.42 | 82.36 | 2.17 | 32.96 | 3.56 |
| PROSPER | 38 | 14.17 | 1.36 | 80.23 | 2.41 | 30.56 | 3.81 |
| RB07 | 208 | 14.56 | 1.03 | 80.98 | 2.76 | 27.98 | 4.66 |
| SELECT | 162 | 14.51 | 1.25 | 82.02 | 3.01 | 27.87 | 3.85 |
| STEELE-ND | 40 | 14.79 | 1.01 | 82.31 | 2.27 | 32.09 | 3.44 |
| TRAVERSE | 129 | 13.43 | 1.18 | 78.32 | 2.58 | 31.20 | 3.21 |
| Average[d] | 1423 | 14.35 | 1.19 | 81.57 | 2.84 | 29.84 | 4.29 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.
[b]N: Sample Size; [c]SD: Standard Deviation; [d]Average: Population Mean.

Table 2.3. County Kernel Quality Trait Averages and Standard Deviations over Analysis Years and Varieties.

| | | GPC[a] (12% moisture basis) | | TWT (kg/hl) | | TKW (grams) | |
|---|---|---|---|---|---|---|---|
| County | N[b] | Average | SD[c] | Average | SD | Average | SD |
| Beadle | 4 | 14.98 | 0.51 | 79.68 | 5.53 | 29.38 | 4.01 |
| Brookings | 71 | 13.76 | 1.42 | 82.04 | 2.42 | 31.31 | 4.21 |
| Brown | 157 | 14.35 | 0.94 | 82.01 | 2.59 | 30.56 | 3.30 |
| Campbell | 18 | 14.63 | 0.69 | 82.50 | 1.94 | 28.80 | 3.79 |
| Charles Mix | 12 | 14.16 | 1.29 | 80.17 | 2.71 | 30.53 | 1.64 |
| Clark | 41 | 14.47 | 1.36 | 82.01 | 2.75 | 30.03 | 4.76 |
| Codington | 24 | 14.43 | 1.15 | 81.68 | 2.74 | 29.80 | 5.20 |
| Corson | 30 | 14.93 | 1.40 | 82.02 | 2.26 | 29.02 | 4.38 |
| Day | 226 | 14.14 | 1.09 | 82.11 | 2.51 | 30.85 | 4.20 |
| Deuel | 16 | 13.91 | 1.12 | 81.18 | 2.99 | 32.33 | 3.01 |
| Dewey | 11 | 14.31 | 1.42 | 80.87 | 2.85 | 28.42 | 5.12 |
| Douglas | 1 | 13.60 | - | 81.14 | - | 34.50 | - |
| Edmunds | 45 | 14.24 | 0.90 | 81.85 | 2.04 | 28.80 | 3.92 |
| Faulk | 57 | 14.89 | 1.00 | 81.05 | 3.00 | 30.99 | 4.07 |
| Grant | 14 | 13.50 | 0.86 | 82.74 | 2.96 | 35.16 | 5.15 |
| Hamlin | 7 | 14.09 | 0.64 | 83.57 | 1.45 | 33.00 | 1.85 |
| Hand | 85 | 14.78 | 1.17 | 80.59 | 2.94 | 28.45 | 3.44 |
| Hanson | 2 | 14.95 | 1.48 | 77.45 | 8.50 | 27.80 | 5.09 |
| Hughes | 7 | 15.04 | 1.10 | 82.04 | 2.20 | 26.09 | 3.66 |
| Hutchinson | 3 | 15.23 | 0.23 | 77.69 | 6.64 | 28.30 | 2.34 |
| Hyde | 7 | 14.29 | 0.86 | 81.38 | 4.09 | 26.61 | 3.38 |
| Jerauld | 17 | 13.86 | 1.53 | 80.95 | 4.19 | 29.35 | 3.39 |
| Jones | 23 | 13.85 | 0.96 | 80.36 | 3.89 | 27.07 | 4.66 |
| Kingsbury | 7 | 14.14 | 0.91 | 81.12 | 4.11 | 29.61 | 4.59 |
| Lake | 18 | 14.32 | 0.96 | 80.04 | 3.24 | 32.61 | 3.69 |
| Lyman | 8 | 13.70 | 2.00 | 82.09 | 3.32 | 28.33 | 2.65 |
| Marshall | 16 | 14.53 | 1.04 | 82.09 | 2.31 | 33.30 | 1.74 |
| McPherson | 50 | 14.63 | 1.13 | 81.09 | 2.82 | 29.47 | 4.23 |
| Minnehaha | 1 | 12.20 | - | 80.62 | - | 29.50 | - |
| Moody | 1 | 16.40 | - | 82.30 | - | 28.40 | - |
| Pennington | 6 | 14.32 | 2.07 | 82.26 | 2.81 | 30.85 | 2.38 |
| Potter | 80 | 14.76 | 1.18 | 81.32 | 2.68 | 29.21 | 5.01 |
| Roberts | 28 | 14.04 | 1.04 | 82.69 | 3.19 | 31.17 | 4.48 |
| Sanborn | 1 | 14.40 | - | 78.68 | - | 33.60 | - |
| Spink | 76 | 14.08 | 1.36 | 81.05 | 3.06 | 29.15 | 4.36 |
| Sully | 31 | 14.90 | 1.25 | 82.88 | 2.24 | 28.33 | 3.12 |
| Tripp | 24 | 14.60 | 1.12 | 79.14 | 3.82 | 27.29 | 3.50 |
| Walworth | 198 | 14.31 | 1.18 | 81.45 | 2.64 | 28.73 | 4.50 |
| Average[d] | 1423 | 14.35 | 1.19 | 81.57 | 2.84 | 29.84 | 4.29 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.4. District Kernel Quality Trait Averages and Standard Deviations over Analysis Years and Varieties.

| | | GPC[a] (12% moisture basis) | | TWT (kg/hl) | | TKW (grams) | |
|---|---|---|---|---|---|---|---|
| District | N[b] | Average | SD[c] | Average | SD | Average | SD |
| Central | 144 | 14.68 | 1.24 | 81.14 | 3.22 | 28.46 | 3.38 |
| East Central | 107 | 14.02 | 1.35 | 81.53 | 2.90 | 31.01 | 4.31 |
| North Central | 681 | 14.42 | 1.13 | 81.51 | 2.69 | 29.50 | 4.25 |
| North East | 372 | 14.17 | 1.12 | 82.12 | 2.62 | 31.09 | 4.36 |
| North West | 41 | 14.76 | 1.42 | 81.71 | 2.45 | 28.86 | 4.53 |
| South Central | 56 | 14.16 | 1.25 | 80.12 | 3.83 | 27.43 | 3.90 |
| South East | 16 | 14.33 | 1.20 | 79.76 | 3.52 | 30.36 | 2.17 |
| West Central | 6 | 14.32 | 2.07 | 82.26 | 2.81 | 30.85 | 2.38 |
| Average[d] | 1423 | 14.35 | 1.19 | 81.57 | 2.84 | 29.84 | 4.29 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.5. Year Kernel Quality Trait Averages and Standard Deviations over Analysis Varieties and Production Environments.

| | | GPC[a] (12% moisture basis) | | TWT (kg/hl) | | TKW (grams) | |
|---|---|---|---|---|---|---|---|
| Year | **N[b]** | Average | SD[c] | Average | SD | Average | SD |
| 2008 | 19 | 14.27 | 1.32 | 81.01 | 1.77 | 31.82 | 2.29 |
| 2009 | 348 | 14.12 | 1.14 | 81.35 | 2.54 | 32.53 | 2.89 |
| 2010 | 252 | 14.16 | 1.17 | 81.88 | 2.72 | 32.96 | 3.52 |
| 2011 | 163 | 14.90 | 1.09 | 80.27 | 3.19 | 25.67 | 3.76 |
| 2012 | 402 | 14.57 | 1.17 | 81.51 | 3.04 | 27.56 | 3.49 |
| 2013 | 199 | 14.26 | 1.15 | 82.48 | 2.47 | 28.61 | 3.17 |
| 2015 | 40 | 13.49 | 0.98 | 83.19 | 1.81 | 31.91 | 3.23 |
| Average[d] | 1423 | 14.35 | 1.19 | 81.57 | 2.84 | 29.84 | 4.29 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.6. Variety Flour Quality Trait Averages and Standard Deviations over Analysis Years and Production Environments.

| | | EXT[a] (%) | | ASH (14% moisture basis) | | FPC (14% moisture basis) | | GI | | WGC (%) | | DGC (%) | | WB (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| ADVANCE | 68 | 57.99 | 2.68 | 0.31 | 0.03 | 13.72 | 1.02 | 97.64 | 2.19 | 32.58 | 2.88 | 11.82 | 1.04 | 20.77 | 1.88 |
| BARLOW | 89 | 57.48 | 2.25 | 0.30 | 0.02 | 14.88 | 0.89 | 93.45 | 4.09 | 37.11 | 2.93 | 13.44 | 1.23 | 23.67 | 1.98 |
| BRICK | 209 | 58.17 | 2.93 | 0.29 | 0.03 | 14.15 | 1.03 | 97.49 | 2.72 | 34.53 | 3.71 | 12.76 | 1.41 | 21.77 | 2.44 |
| BRIGGS | 287 | 60.05 | 2.68 | 0.28 | 0.03 | 14.47 | 1.16 | 83.04 | 8.82 | 38.02 | 4.02 | 13.31 | 1.42 | 24.71 | 2.76 |
| FALLER | 106 | 58.52 | 3.10 | 0.33 | 0.03 | 14.10 | 0.94 | 94.46 | 4.86 | 35.14 | 3.48 | 12.48 | 1.13 | 22.66 | 2.40 |
| FOREFRONT | 44 | 58.76 | 2.07 | 0.26 | 0.03 | 13.78 | 1.15 | 96.25 | 3.20 | 33.30 | 3.80 | 11.80 | 1.28 | 21.50 | 2.55 |
| HOWARD | 43 | 61.59 | 2.52 | 0.28 | 0.03 | 13.94 | 1.53 | 90.67 | 7.82 | 36.54 | 5.43 | 12.87 | 1.83 | 23.67 | 3.65 |
| PROSPER | 38 | 58.42 | 2.73 | 0.33 | 0.04 | 14.01 | 1.35 | 92.17 | 8.70 | 35.17 | 4.84 | 12.45 | 1.60 | 22.72 | 3.43 |
| RB07 | 208 | 59.95 | 2.80 | 0.27 | 0.03 | 14.39 | 0.93 | 92.73 | 6.32 | 36.82 | 3.54 | 13.39 | 1.38 | 23.43 | 2.41 |
| SELECT | 162 | 56.01 | 2.71 | 0.34 | 0.03 | 14.30 | 1.20 | 93.31 | 5.81 | 35.44 | 3.79 | 12.65 | 1.34 | 22.79 | 2.52 |
| STEELE-ND | 40 | 60.33 | 2.64 | 0.30 | 0.03 | 14.94 | 0.97 | 91.98 | 6.18 | 38.41 | 3.23 | 13.66 | 1.21 | 24.75 | 2.21 |
| TRAVERSE | 129 | 59.10 | 2.20 | 0.31 | 0.03 | 13.28 | 1.18 | 71.30 | 13.39 | 37.16 | 4.65 | 12.79 | 1.60 | 24.37 | 3.12 |
| Average[d] | 1423 | 58.81 | 3.02 | 0.30 | 0.04 | 14.21 | 1.16 | 90.02 | 10.45 | 36.17 | 4.14 | 12.92 | 1.46 | 23.25 | 2.85 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.7. County Flour Quality Trait Averages and Standard Deviations over Analysis Years and Varieties.

| | | EXT[a] (%) | | ASH (14% moisture basis) | | FPC (14% moisture basis) | | GI | | WGC (%) | | DGC (%) | | WB (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| Beadle | 4 | 61.32 | 5.43 | 0.34 | 0.02 | 14.67 | 0.46 | 81.82 | 20.92 | 38.57 | 3.02 | 13.67 | 0.57 | 24.91 | 2.52 |
| Brookings | 71 | 59.44 | 2.97 | 0.29 | 0.04 | 13.62 | 1.37 | 93.39 | 6.71 | 34.39 | 4.41 | 12.43 | 1.55 | 21.96 | 3.05 |
| Brown | 157 | 58.20 | 2.95 | 0.30 | 0.04 | 14.25 | 0.88 | 88.95 | 10.76 | 36.28 | 3.66 | 12.87 | 1.31 | 23.41 | 2.53 |
| Campbell | 18 | 57.86 | 2.33 | 0.29 | 0.03 | 14.33 | 0.60 | 86.86 | 8.83 | 37.52 | 2.46 | 13.10 | 0.62 | 24.41 | 1.88 |
| Charles Mix | 12 | 58.74 | 2.66 | 0.33 | 0.04 | 14.05 | 1.46 | 76.08 | 18.59 | 37.71 | 4.90 | 12.93 | 1.53 | 24.78 | 3.45 |
| Clark | 41 | 58.80 | 3.38 | 0.29 | 0.03 | 14.33 | 1.22 | 91.18 | 9.65 | 36.10 | 3.91 | 12.92 | 1.39 | 23.18 | 2.60 |
| Codington | 24 | 56.88 | 3.60 | 0.28 | 0.03 | 14.17 | 1.14 | 89.63 | 13.04 | 35.68 | 4.38 | 12.78 | 1.51 | 22.90 | 2.97 |
| Corson | 30 | 58.48 | 2.86 | 0.31 | 0.04 | 14.82 | 1.32 | 87.59 | 10.10 | 38.81 | 5.68 | 13.93 | 2.48 | 24.88 | 3.47 |
| Day | 226 | 59.37 | 2.84 | 0.29 | 0.04 | 13.99 | 1.08 | 92.72 | 8.22 | 35.15 | 3.89 | 12.59 | 1.37 | 22.56 | 2.69 |
| Deuel | 16 | 60.14 | 2.73 | 0.28 | 0.03 | 13.83 | 1.09 | 86.53 | 16.19 | 36.40 | 2.95 | 13.01 | 0.98 | 23.39 | 2.09 |
| Dewey | 11 | 56.26 | 3.31 | 0.32 | 0.05 | 14.24 | 1.34 | 90.22 | 9.67 | 36.12 | 3.28 | 13.05 | 1.25 | 23.07 | 2.52 |
| Douglas | 1 | 61.57 | - | 0.23 | - | 13.31 | - | 94.67 | - | 32.73 | - | 11.81 | - | 20.91 | - |
| Edmunds | 45 | 58.97 | 2.79 | 0.28 | 0.03 | 13.96 | 0.91 | 86.58 | 10.38 | 36.27 | 3.21 | 12.73 | 1.03 | 23.55 | 2.31 |
| Faulk | 57 | 59.82 | 2.76 | 0.31 | 0.04 | 14.91 | 0.97 | 88.14 | 9.98 | 39.06 | 4.22 | 13.90 | 1.41 | 25.16 | 2.88 |
| Grant | 14 | 60.28 | 3.34 | 0.26 | 0.03 | 13.26 | 0.78 | 94.57 | 4.58 | 33.30 | 2.72 | 11.83 | 0.92 | 21.47 | 1.90 |
| Hamlin | 7 | 58.98 | 3.01 | 0.31 | 0.05 | 14.08 | 0.60 | 93.83 | 4.21 | 35.66 | 2.50 | 12.67 | 0.81 | 22.98 | 1.75 |
| Hand | 85 | 58.16 | 3.19 | 0.30 | 0.03 | 14.46 | 1.03 | 85.95 | 13.20 | 37.14 | 4.22 | 13.15 | 1.30 | 23.99 | 3.07 |
| Hanson | 2 | 59.93 | 6.56 | 0.35 | 0.02 | 14.70 | 0.42 | 75.28 | 1.77 | 38.12 | 1.13 | 13.16 | 0.11 | 24.96 | 1.03 |
| Hughes | 7 | 59.82 | 3.38 | 0.31 | 0.01 | 15.01 | 1.29 | 95.08 | 7.37 | 36.91 | 5.73 | 13.62 | 1.71 | 23.29 | 4.04 |
| Hutchinson | 3 | 57.86 | 3.24 | 0.35 | 0.01 | 14.97 | 0.25 | 84.24 | 23.62 | 38.31 | 3.42 | 13.88 | 0.45 | 24.43 | 2.97 |
| Hyde | 7 | 57.47 | 2.59 | 0.31 | 0.04 | 14.03 | 0.81 | 94.55 | 4.84 | 34.88 | 3.28 | 12.46 | 1.09 | 22.42 | 2.21 |
| Jerauld | 17 | 56.65 | 3.26 | 0.32 | 0.03 | 13.42 | 1.41 | 92.20 | 8.97 | 33.31 | 4.37 | 11.89 | 1.50 | 21.42 | 3.03 |
| Jones | 23 | 57.11 | 2.57 | 0.33 | 0.03 | 13.82 | 1.02 | 86.76 | 13.59 | 35.36 | 4.19 | 12.50 | 1.25 | 22.86 | 3.03 |
| Kingsbury | 7 | 60.20 | 2.65 | 0.30 | 0.03 | 13.93 | 0.87 | 91.75 | 9.84 | 34.87 | 3.70 | 12.51 | 1.27 | 22.36 | 2.52 |
| Lake | 18 | 58.79 | 2.91 | 0.29 | 0.03 | 14.19 | 0.99 | 78.42 | 14.00 | 38.22 | 3.65 | 13.32 | 1.34 | 24.91 | 2.40 |
| Lyman | 8 | 57.39 | 3.11 | 0.32 | 0.04 | 13.67 | 2.12 | 92.54 | 5.39 | 34.26 | 7.25 | 12.09 | 2.54 | 22.18 | 4.73 |
| Marshall | 16 | 60.08 | 2.12 | 0.28 | 0.02 | 14.42 | 1.15 | 83.65 | 13.84 | 37.51 | 3.49 | 13.24 | 1.19 | 24.27 | 2.43 |
| McPherson | 50 | 59.17 | 2.50 | 0.30 | 0.03 | 14.58 | 1.03 | 87.56 | 12.08 | 38.29 | 3.34 | 13.68 | 1.25 | 24.61 | 2.29 |
| Minnehaha | 1 | 59.57 | - | 0.30 | - | 11.91 | - | 77.91 | - | 33.31 | - | 11.62 | - | 21.69 | - |
| Moody | 1 | 55.86 | - | 0.28 | - | 16.09 | - | 95.38 | - | 40.18 | - | 14.47 | - | 25.71 | - |
| Pennington | 6 | 55.83 | 1.70 | 0.31 | 0.04 | 14.22 | 2.24 | 87.82 | 13.42 | 36.76 | 5.93 | 12.96 | 2.28 | 23.80 | 3.72 |
| Potter | 80 | 58.61 | 2.88 | 0.29 | 0.04 | 14.66 | 1.13 | 88.91 | 8.72 | 37.47 | 3.78 | 13.33 | 1.25 | 24.13 | 2.72 |
| Roberts | 28 | 58.62 | 3.26 | 0.28 | 0.03 | 13.85 | 0.98 | 93.21 | 5.93 | 34.44 | 3.07 | 12.38 | 1.10 | 22.05 | 2.04 |
| Sanborn | 1 | 59.57 | - | 0.30 | - | 14.19 | - | 76.24 | - | 39.25 | - | 13.60 | - | 25.65 | - |
| Spink | 76 | 59.17 | 3.09 | 0.30 | 0.04 | 13.97 | 1.38 | 91.30 | 9.68 | 34.92 | 4.55 | 12.57 | 1.64 | 22.35 | 3.10 |
| Sully | 31 | 58.22 | 3.38 | 0.31 | 0.03 | 14.88 | 1.18 | 90.77 | 10.25 | 37.72 | 3.97 | 13.67 | 1.55 | 24.05 | 2.89 |
| Tripp | 24 | 57.86 | 2.53 | 0.33 | 0.04 | 14.46 | 1.22 | 84.05 | 13.30 | 37.24 | 3.72 | 13.14 | 1.35 | 24.09 | 2.50 |
| Walworth | 198 | 59.12 | 2.92 | 0.29 | 0.04 | 14.20 | 1.15 | 93.29 | 7.67 | 35.66 | 3.92 | 12.88 | 1.46 | 22.78 | 2.60 |
| Average[d] | 1423 | 58.81 | 3.02 | 0.30 | 0.04 | 14.21 | 1.16 | 90.02 | 10.45 | 36.17 | 4.14 | 12.92 | 1.46 | 23.25 | 2.85 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.8. District Flour Quality Trait Averages and Standard Deviations over Analysis Years and Varieties.

| | | EXT[a] (%) | | ASH (14% moisture basis) | | FPC (14% moisture basis) | | GI | | WGC (%) | | DGC (%) | | WB (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| Central | 144 | 58.05 | 3.32 | 0.31 | 0.03 | 14.41 | 1.16 | 88.03 | 12.37 | 36.74 | 4.30 | 13.09 | 1.45 | 23.65 | 3.08 |
| East Central | 107 | 59.38 | 2.98 | 0.29 | 0.04 | 13.88 | 1.32 | 90.39 | 10.40 | 35.40 | 4.51 | 12.70 | 1.53 | 22.70 | 3.14 |
| North Central | 681 | 58.87 | 2.90 | 0.30 | 0.04 | 14.31 | 1.10 | 90.06 | 9.80 | 36.49 | 4.00 | 13.03 | 1.41 | 23.46 | 2.74 |
| North East | 372 | 59.18 | 3.04 | 0.28 | 0.03 | 14.01 | 1.09 | 91.82 | 9.43 | 35.33 | 3.80 | 12.64 | 1.33 | 22.69 | 2.61 |
| North West | 41 | 57.88 | 3.11 | 0.31 | 0.04 | 14.66 | 1.33 | 88.30 | 9.93 | 38.09 | 5.25 | 13.69 | 2.24 | 24.40 | 3.31 |
| South Central | 56 | 57.58 | 2.69 | 0.33 | 0.04 | 14.10 | 1.32 | 86.57 | 12.68 | 36.06 | 4.57 | 12.74 | 1.54 | 23.32 | 3.11 |
| South East | 16 | 58.75 | 2.70 | 0.32 | 0.05 | 14.17 | 1.33 | 78.77 | 18.88 | 37.51 | 4.56 | 13.04 | 1.42 | 24.47 | 3.29 |
| West Central | 6 | 55.83 | 1.70 | 0.31 | 0.04 | 14.22 | 2.24 | 87.82 | 13.42 | 36.76 | 5.93 | 12.96 | 2.28 | 23.80 | 3.72 |
| Average[d] | 1423 | 58.81 | 3.02 | 0.30 | 0.04 | 14.21 | 1.16 | 90.02 | 10.45 | 36.17 | 4.14 | 12.92 | 1.46 | 23.25 | 2.85 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.9. Year Flour Quality Trait Averages and Standard Deviations over Analysis Varieties and Production Environments.

| | | EXT[a] (%) | | ASH (14% moisture basis) | | FPC (14% moisture basis) | | GI | | WGC (%) | | DGC (%) | | WB (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| 2008 | 19 | 61.05 | 2.30 | 0.27 | 0.02 | 14.15 | 1.30 | 89.52 | 10.14 | 36.92 | 4.57 | 13.20 | 1.78 | 23.72 | 2.91 |
| 2009 | 348 | 60.77 | 2.43 | 0.28 | 0.03 | 14.09 | 1.18 | 85.60 | 11.88 | 37.28 | 3.98 | 13.23 | 1.40 | 24.04 | 2.80 |
| 2010 | 252 | 60.47 | 2.33 | 0.29 | 0.03 | 14.17 | 1.21 | 85.56 | 12.83 | 37.52 | 4.29 | 13.30 | 1.59 | 24.23 | 2.87 |
| 2011 | 163 | 56.79 | 2.74 | 0.30 | 0.03 | 14.56 | 1.00 | 91.71 | 7.68 | 36.56 | 3.43 | 13.07 | 1.14 | 23.49 | 2.41 |
| 2012 | 402 | 57.39 | 2.52 | 0.31 | 0.04 | 14.35 | 1.12 | 93.29 | 7.58 | 35.44 | 3.94 | 12.78 | 1.43 | 22.66 | 2.70 |
| 2013 | 199 | 57.55 | 2.79 | 0.31 | 0.04 | 14.09 | 1.14 | 94.42 | 6.50 | 34.40 | 3.90 | 12.31 | 1.30 | 22.08 | 2.68 |
| 2015 | 40 | 59.07 | 2.18 | 0.28 | 0.03 | 13.24 | 1.07 | 95.01 | 4.52 | 32.30 | 3.31 | 11.46 | 1.16 | 20.84 | 2.20 |
| Average[d] | 1423 | 58.81 | 3.02 | 0.30 | 0.04 | 14.21 | 1.16 | 90.02 | 10.45 | 36.17 | 4.14 | 12.92 | 1.46 | 23.25 | 2.85 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.10. Variety Dough Quality Trait Averages and Standard Deviations over Analysis Years and Production Environments.

| | | ABS[a] (%) | | EPT (minutes) | | EPV (%) | | ELS (%) | | ERS (%) | | MSE (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| ADVANCE | 68 | 64.18 | 1.53 | 4.41 | 0.89 | 72.93 | 4.01 | 19.94 | 7.56 | -10.98 | 2.71 | 30.92 | 8.06 |
| BARLOW | 89 | 65.91 | 1.33 | 3.81 | 0.65 | 77.52 | 4.07 | 28.04 | 12.35 | -11.05 | 2.56 | 39.10 | 12.66 |
| BRICK | 209 | 64.83 | 1.54 | 4.94 | 1.14 | 75.64 | 4.73 | 22.42 | 9.82 | -11.14 | 3.03 | 33.57 | 10.40 |
| BRIGGS | 287 | 65.30 | 1.74 | 2.63 | 0.82 | 75.39 | 4.99 | 19.53 | 13.52 | -11.22 | 2.88 | 30.75 | 13.88 |
| FALLER | 106 | 64.75 | 1.42 | 3.90 | 0.98 | 75.63 | 4.71 | 25.27 | 11.39 | -11.02 | 2.90 | 36.29 | 11.64 |
| FOREFRONT | 44 | 64.26 | 1.73 | 4.14 | 0.98 | 72.59 | 4.05 | 20.92 | 9.05 | -11.67 | 3.17 | 32.61 | 9.63 |
| HOWARD | 43 | 64.51 | 2.30 | 3.18 | 0.85 | 77.92 | 5.54 | 24.51 | 16.03 | -11.19 | 2.94 | 35.71 | 16.73 |
| PROSPER | 38 | 64.62 | 2.03 | 3.74 | 1.03 | 72.21 | 4.18 | 23.03 | 13.86 | -12.70 | 5.30 | 35.74 | 13.92 |
| RB07 | 208 | 65.19 | 1.39 | 3.49 | 0.90 | 75.96 | 4.35 | 22.34 | 8.94 | -11.9 | 2.81 | 34.24 | 9.28 |
| SELECT | 162 | 65.05 | 1.80 | 3.95 | 1.03 | 73.52 | 4.67 | 26.02 | 12.20 | -10.84 | 3.05 | 36.85 | 12.35 |
| STEELE-ND | 40 | 66.01 | 1.46 | 3.29 | 0.69 | 79.49 | 3.82 | 27.71 | 15.87 | -11.11 | 2.64 | 38.81 | 16.46 |
| TRAVERSE | 129 | 63.52 | 1.76 | 2.40 | 0.71 | 73.55 | 5.62 | 23.63 | 15.74 | -13.53 | 3.92 | 37.16 | 16.81 |
| Average[d] | 1423 | 64.91 | 1.74 | 3.59 | 1.22 | 75.18 | 4.95 | 22.97 | 12.34 | -11.49 | 3.17 | 34.46 | 12.79 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.11. Variety Dough Quality Trait Averages and Standard Deviations over Analysis Years and Production Environments (con't).

| | | MPT[a] (minutes) | | MPV (%) | | MLS (%) | | MRS (%) | | MSM (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD |
| ADVANCE | 68 | 5.13 | 0.81 | 53.45 | 3.29 | 4.91 | 2.49 | -1.48 | 1.02 | 6.44 | 2.64 |
| BARLOW | 89 | 4.54 | 0.61 | 57.29 | 3.58 | 5.26 | 2.24 | -1.52 | 0.93 | 6.82 | 2.23 |
| BRICK | 209 | 5.73 | 1.18 | 55.00 | 3.94 | 4.73 | 3.11 | -1.20 | 1.10 | 6.04 | 3.39 |
| BRIGGS | 287 | 3.37 | 0.79 | 56.81 | 4.13 | 6.77 | 3.30 | -2.53 | 1.32 | 9.32 | 3.89 |
| FALLER | 106 | 4.55 | 1.00 | 55.59 | 3.45 | 6.09 | 2.32 | -1.18 | 1.07 | 7.39 | 2.67 |
| FOREFRONT | 44 | 4.82 | 0.88 | 53.64 | 3.39 | 5.89 | 2.91 | -1.68 | 0.98 | 7.61 | 3.20 |
| HOWARD | 43 | 3.88 | 0.75 | 57.52 | 4.68 | 5.86 | 2.86 | -1.84 | 1.13 | 7.74 | 3.32 |
| PROSPER | 38 | 4.46 | 1.02 | 52.45 | 4.02 | 5.30 | 3.25 | -1.45 | 1.45 | 6.90 | 4.06 |
| RB07 | 208 | 4.32 | 0.91 | 56.36 | 3.79 | 6.12 | 3.10 | -2.35 | 1.51 | 8.52 | 3.64 |
| SELECT | 162 | 4.85 | 0.97 | 54.35 | 3.83 | 4.36 | 2.95 | -1.41 | 1.25 | 5.87 | 3.29 |
| STEELE-ND | 40 | 3.98 | 0.63 | 58.76 | 3.52 | 5.78 | 2.41 | -1.84 | 1.10 | 7.67 | 2.86 |
| TRAVERSE | 129 | 3.24 | 0.89 | 55.39 | 4.40 | 7.01 | 4.29 | -3.85 | 1.72 | 10.93 | 5.45 |
| Average[d] | 1423 | 4.36 | 1.22 | 55.71 | 4.11 | 5.77 | 3.22 | -1.99 | 1.50 | 7.82 | 3.94 |

[a]MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.12. County Dough Quality Trait Averages and Standard Deviations over Analysis Years and Varieties.

| | | ABS[a] (%) | | EPT (minutes) | | EPV (%) | | ELS (%) | | ERS (%) | | MSE (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| Beadle | 4 | 65.60 | 0.70 | 2.71 | 0.95 | 69.28 | 7.29 | 15.27 | 10.52 | -12.67 | 5.72 | 27.93 | 9.86 |
| Brookings | 71 | 64.03 | 2.06 | 3.54 | 1.28 | 76.04 | 4.74 | 21.62 | 14.06 | -11.85 | 2.89 | 33.48 | 14.64 |
| Brown | 157 | 64.97 | 1.33 | 3.46 | 1.12 | 75.34 | 4.16 | 23.61 | 12.50 | -11.71 | 3.82 | 35.33 | 12.94 |
| Campbell | 18 | 65.09 | 0.90 | 3.38 | 1.14 | 73.17 | 3.82 | 21.18 | 10.52 | -10.42 | 1.83 | 31.59 | 11.06 |
| Charles Mix | 12 | 64.67 | 2.20 | 2.57 | 0.56 | 73.91 | 7.36 | 30.73 | 22.06 | -11.77 | 3.61 | 42.51 | 22.54 |
| Clark | 41 | 65.09 | 1.83 | 3.74 | 1.60 | 74.96 | 5.71 | 24.40 | 13.44 | -11.16 | 2.78 | 35.56 | 13.25 |
| Codington | 24 | 64.86 | 1.70 | 4.23 | 1.46 | 75.19 | 4.61 | 24.69 | 10.03 | -11.84 | 3.71 | 36.53 | 9.56 |
| Corson | 30 | 65.83 | 1.98 | 3.59 | 1.46 | 75.89 | 5.02 | 22.77 | 13.25 | -11.47 | 2.72 | 34.23 | 12.85 |
| Day | 226 | 64.58 | 1.62 | 3.77 | 1.14 | 75.55 | 4.81 | 22.19 | 10.59 | -11.45 | 3.34 | 33.64 | 11.00 |
| Deuel | 16 | 64.34 | 1.63 | 3.08 | 1.00 | 76.34 | 4.96 | 17.66 | 10.17 | -12.38 | 3.17 | 30.10 | 9.98 |
| Dewey | 11 | 64.97 | 2.01 | 3.76 | 1.21 | 76.31 | 5.40 | 27.36 | 14.96 | -10.48 | 1.51 | 37.84 | 15.24 |
| Douglas | 1 | 63.57 | - | 3.11 | - | 67.99 | - | 8.84 | - | -11.44 | - | 20.28 | - |
| Edmunds | 45 | 64.54 | 1.36 | 3.42 | 1.27 | 73.84 | 4.36 | 21.54 | 11.35 | -11.16 | 2.79 | 32.70 | 11.02 |
| Faulk | 57 | 65.97 | 1.45 | 3.50 | 1.21 | 77.93 | 4.46 | 24.14 | 14.98 | -11.46 | 2.77 | 35.61 | 15.98 |
| Grant | 14 | 63.49 | 1.18 | 3.35 | 0.85 | 74.41 | 3.95 | 25.60 | 12.35 | -12.28 | 2.85 | 37.89 | 11.80 |
| Hamlin | 7 | 64.72 | 0.90 | 3.66 | 0.73 | 75.98 | 3.70 | 25.44 | 8.70 | -11.53 | 1.52 | 36.97 | 8.51 |
| Hand | 85 | 65.29 | 1.55 | 3.36 | 0.97 | 74.51 | 4.91 | 23.88 | 11.45 | -11.68 | 3.00 | 35.56 | 11.82 |
| Hanson | 2 | 65.66 | 0.63 | 1.74 | 0.62 | 75.49 | 0.21 | 9.94 | 14.02 | -11.11 | 1.17 | 21.06 | 12.85 |
| Hughes | 7 | 66.10 | 1.94 | 4.12 | 1.11 | 76.65 | 3.66 | 22.12 | 5.75 | -12.23 | 4.11 | 34.35 | 6.72 |
| Hutchinson | 3 | 66.05 | 0.38 | 2.94 | 1.05 | 79.39 | 8.66 | 20.29 | 3.28 | -12.45 | 2.95 | 32.74 | 6.22 |
| Hyde | 7 | 64.64 | 1.21 | 4.51 | 0.99 | 71.57 | 3.34 | 16.36 | 2.93 | -10.32 | 2.63 | 26.68 | 3.57 |
| Jerauld | 17 | 63.73 | 2.12 | 3.60 | 0.91 | 71.98 | 3.64 | 24.47 | 13.74 | -11.48 | 3.13 | 35.95 | 13.90 |
| Jones | 23 | 64.34 | 1.53 | 3.63 | 1.36 | 73.25 | 3.82 | 23.50 | 13.33 | -11.48 | 3.22 | 34.98 | 14.06 |
| Kingsbury | 7 | 64.49 | 1.30 | 3.63 | 1.20 | 75.22 | 2.78 | 28.13 | 19.59 | -11.29 | 2.17 | 39.42 | 18.76 |
| Lake | 18 | 64.88 | 1.49 | 2.51 | 0.83 | 75.30 | 4.36 | 30.48 | 19.67 | -12.03 | 3.37 | 42.51 | 19.64 |
| Lyman | 8 | 64.10 | 3.19 | 2.95 | 1.20 | 70.88 | 7.26 | 25.27 | 6.09 | -9.49 | 1.93 | 34.76 | 5.76 |
| Marshall | 16 | 65.23 | 1.72 | 2.96 | 1.14 | 76.07 | 5.61 | 23.52 | 15.20 | -11.50 | 2.83 | 35.02 | 16.11 |
| McPherson | 50 | 65.47 | 1.55 | 3.02 | 0.87 | 77.60 | 4.58 | 24.68 | 15.08 | -11.25 | 2.16 | 35.93 | 15.35 |
| Minnehaha | 1 | 61.47 | - | 2.50 | - | 76.89 | - | 21.33 | - | -15.06 | - | 36.38 | - |
| Moody | 1 | 67.74 | - | 5.47 | - | 73.89 | - | 23.28 | - | -11.11 | - | 34.39 | -! |
| Pennington | 6 | 64.93 | 3.37 | 3.66 | 0.56 | 74.06 | 8.43 | 34.61 | 19.08 | -13.64 | 8.58 | 48.24 | 17.41 |
| Potter | 80 | 65.59 | 1.69 | 3.54 | 1.32 | 75.29 | 4.79 | 23.26 | 12.43 | -11.45 | 2.88 | 34.71 | 13.12 |
| Roberts | 28 | 64.37 | 1.47 | 3.79 | 1.54 | 74.46 | 4.36 | 24.64 | 12.61 | -11.44 | 3.23 | 36.08 | 13.43 |
| Sanborn | 1 | 64.89 | - | 2.01 | - | 75.07 | - | 22.62 | - | -11.54 | - | 34.17 | - |
| Spink | 76 | 64.56 | 2.07 | 3.82 | 1.24 | 73.68 | 5.68 | 20.66 | 11.63 | -11.75 | 3.73 | 32.41 | 12.90 |
| Sully | 31 | 65.91 | 1.77 | 3.77 | 1.24 | 75.71 | 5.40 | 21.48 | 9.01 | -11.48 | 3.42 | 32.96 | 10.06 |
| Tripp | 24 | 65.30 | 1.83 | 3.33 | 1.22 | 74.48 | 5.63 | 22.35 | 10.31 | -10.67 | 2.47 | 33.02 | 10.20 |
| Walworth | 198 | 64.90 | 1.72 | 3.89 | 1.25 | 75.02 | 5.07 | 22.10 | 11.15 | -11.28 | 2.95 | 33.38 | 11.83 |
| Average[d] | 1423 | 64.91 | 1.74 | 3.59 | 1.22 | 75.18 | 4.95 | 22.97 | 12.34 | -11.49 | 3.17 | 34.46 | 12.79 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability.

[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.13. County Dough Quality Trait Averages and Standard Deviations over Analysis Years and Varieties (con't).

| | | MPT[a] (minutes) | | MPV (%) | | MLS (%) | | MRS (%) | | MSM (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD |
| Beadle | 4 | 3.92 | 0.83 | 52.52 | 5.35 | 5.64 | 4.74 | -3.01 | 2.35 | 9.14 | 5.92 |
| Brookings | 71 | 4.31 | 1.34 | 55.84 | 4.31 | 6.43 | 4.28 | -2.03 | 1.70 | 8.55 | 5.33 |
| Brown | 157 | 4.15 | 1.14 | 56.23 | 3.64 | 6.50 | 3.17 | -2.08 | 1.72 | 8.67 | 4.24 |
| Campbell | 18 | 4.45 | 1.16 | 54.84 | 2.94 | 4.99 | 2.73 | -2.64 | 1.46 | 7.63 | 2.98 |
| Charles Mix | 12 | 3.48 | 0.94 | 54.96 | 4.42 | 5.67 | 4.41 | -3.22 | 1.29 | 8.96 | 5.27 |
| Clark | 41 | 4.64 | 1.72 | 55.92 | 4.40 | 5.24 | 2.52 | -2.07 | 1.55 | 7.35 | 3.57 |
| Codington | 24 | 4.91 | 1.46 | 55.54 | 4.76 | 5.77 | 3.87 | -1.54 | 1.41 | 7.45 | 4.45 |
| Corson | 30 | 4.40 | 1.36 | 55.79 | 4.20 | 4.37 | 2.67 | -2.17 | 1.17 | 6.58 | 3.12 |
| Day | 226 | 4.52 | 1.16 | 55.70 | 4.25 | 5.33 | 2.80 | -1.69 | 1.30 | 7.07 | 3.18 |
| Deuel | 16 | 3.89 | 0.93 | 56.85 | 2.93 | 6.37 | 3.23 | -2.55 | 2.22 | 8.96 | 4.36 |
| Dewey | 11 | 4.56 | 1.16 | 57.48 | 4.18 | 5.88 | 3.32 | -1.93 | 0.99 | 7.92 | 3.36 |
| Douglas | 1 | 3.54 | - | 49.52 | - | 2.13 | - | -2.10 | - | 4.24 | - |
| Edmunds | 45 | 4.17 | 1.17 | 54.85 | 3.59 | 5.47 | 2.81 | -1.70 | 1.18 | 7.19 | 2.89 |
| Faulk | 57 | 4.30 | 1.35 | 58.13 | 4.05 | 7.06 | 4.52 | -2.54 | 1.73 | 9.65 | 5.63 |
| Grant | 14 | 4.17 | 0.71 | 54.94 | 2.71 | 5.71 | 1.93 | -2.10 | 1.19 | 7.81 | 2.44 |
| Hamlin | 7 | 4.44 | 0.83 | 53.66 | 1.95 | 5.09 | 1.90 | -1.26 | 0.65 | 6.34 | 1.94 |
| Hand | 85 | 4.16 | 0.94 | 55.31 | 4.03 | 5.68 | 3.29 | -2.20 | 1.48 | 7.93 | 3.87 |
| Hanson | 2 | 2.75 | 0.51 | 55.47 | 2.67 | 7.78 | 3.68 | -2.79 | 1.99 | 10.57 | 5.66 |
| Hughes | 7 | 4.60 | 1.19 | 57.47 | 4.55 | 7.35 | 3.54 | -2.96 | 2.53 | 10.31 | 5.59 |
| Hutchinson | 3 | 3.90 | 0.90 | 59.90 | 4.89 | 8.93 | 6.30 | -3.34 | 1.95 | 12.27 | 6.86 |
| Hyde | 7 | 5.20 | 0.83 | 53.92 | 2.65 | 4.17 | 2.93 | -1.62 | 1.00 | 5.79 | 3.30 |
| Jerauld | 17 | 4.68 | 0.87 | 52.49 | 2.81 | 3.07 | 2.51 | -1.40 | 1.16 | 4.60 | 2.78 |
| Jones | 23 | 4.35 | 1.41 | 54.26 | 3.55 | 6.12 | 3.33 | -1.89 | 1.88 | 8.10 | 4.63 |
| Kingsbury | 7 | 4.30 | 1.17 | 55.20 | 2.29 | 6.60 | 2.09 | -1.52 | 1.20 | 8.12 | 2.95 |
| Lake | 18 | 3.41 | 0.95 | 56.25 | 3.63 | 6.93 | 3.41 | -2.89 | 1.59 | 9.82 | 4.11 |
| Lyman | 8 | 4.33 | 1.11 | 54.80 | 5.75 | 4.91 | 3.11 | -2.09 | 2.18 | 7.09 | 4.79 |
| Marshall | 16 | 3.67 | 0.94 | 56.68 | 4.46 | 7.16 | 2.52 | -2.39 | 1.50 | 9.57 | 3.31 |
| McPherson | 50 | 3.92 | 0.87 | 58.20 | 4.10 | 6.31 | 3.00 | -2.70 | 1.63 | 9.04 | 3.64 |
| Minnehaha | 1 | 2.29 | - | 52.06 | - | 6.60 | - | 0.82 | - | 7.42 | - |
| Moody | 1 | 6.47 | - | 54.46 | - | 4.59 | - | -1.64 | - | 6.22 | - |
| Pennington | 6 | 4.29 | 0.89 | 55.48 | 6.64 | 5.70 | 3.35 | -2.06 | 1.12 | 7.76 | 3.95 |
| Potter | 80 | 4.31 | 1.20 | 56.10 | 3.79 | 5.59 | 3.15 | -2.11 | 1.43 | 7.72 | 3.82 |
| Roberts | 28 | 4.68 | 1.42 | 54.89 | 2.91 | 5.28 | 3.04 | -1.64 | 1.21 | 7.08 | 3.17 |
| Sanborn | 1 | 2.74 | - | 54.04 | - | 4.77 | - | -2.62 | - | 7.39 | - |
| Spink | 76 | 4.54 | 1.28 | 54.52 | 4.55 | 5.34 | 2.82 | -1.78 | 1.35 | 7.18 | 3.43 |
| Sully | 31 | 4.42 | 1.16 | 55.95 | 4.03 | 5.93 | 3.55 | -2.18 | 1.65 | 8.30 | 4.15 |
| Tripp | 24 | 4.33 | 1.16 | 55.73 | 4.17 | 5.50 | 4.64 | -2.37 | 1.38 | 7.92 | 5.29 |
| Walworth | 198 | 4.62 | 1.30 | 55.15 | 4.11 | 5.67 | 2.83 | -1.65 | 1.27 | 7.40 | 3.34 |
| Average[d] | 1423 | 4.36 | 1.22 | 55.71 | 4.11 | 5.77 | 3.22 | -1.99 | 1.50 | 7.82 | 3.94 |

[a]MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.14. District Dough Quality Trait Averages and Standard Deviations over Analysis Years and Varieties.

| | | ABS[a] (%) | | EPT (minutes) | | EPV (%) | | ELS (%) | | ERS (%) | | MSE (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| Central | 144 | 65.22 | 1.74 | 3.52 | 1.06 | 74.18 | 5.05 | 22.83 | 11.08 | -11.57 | 3.15 | 34.40 | 11.54 |
| East Central | 107 | 64.41 | 1.98 | 3.38 | 1.28 | 75.86 | 4.39 | 23.38 | 15.29 | -11.85 | 2.94 | 35.23 | 15.60 |
| North Central | 681 | 65.06 | 1.66 | 3.60 | 1.22 | 75.28 | 4.89 | 22.73 | 12.33 | -11.44 | 3.16 | 34.17 | 12.95 |
| North East | 372 | 64.62 | 1.64 | 3.71 | 1.25 | 75.40 | 4.85 | 22.83 | 11.31 | -11.52 | 3.22 | 34.35 | 11.58 |
| North West | 41 | 65.60 | 2.00 | 3.63 | 1.39 | 76.00 | 5.06 | 24.00 | 13.69 | -11.2 | 2.48 | 35.20 | 13.44 |
| South Central | 56 | 64.75 | 1.98 | 3.40 | 1.27 | 73.55 | 5.28 | 23.18 | 11.02 | -10.77 | 2.80 | 33.95 | 11.35 |
| South East | 16 | 64.86 | 2.00 | 2.67 | 0.64 | 74.57 | 7.59 | 27.41 | 20.01 | -11.88 | 3.29 | 39.29 | 20.46 |
| West Central | 6 | 64.93 | 3.37 | 3.66 | 0.56 | 74.06 | 8.43 | 34.61 | 19.08 | -13.64 | 8.58 | 48.24 | 17.41 |
| Averaged[d] | 1423 | 64.91 | 1.74 | 3.59 | 1.22 | 75.18 | 4.95 | 22.97 | 12.34 | -11.49 | 3.17 | 34.46 | 12.79 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.15. District Dough Quality Trait Averages and Standard Deviations over Analysis Years and Varieties (con't).

| | | MPTa (minutes) | | MPV (%) | | MLS (%) | | MRS (%) | | MSM (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD |
| Central | 144 | 4.32 | 1.00 | 54.97 | 4.00 | 5.35 | 3.37 | -2.10 | 1.51 | 7.55 | 3.99 |
| East Central | 107 | 4.15 | 1.31 | 55.94 | 4.03 | 6.58 | 3.90 | -2.22 | 1.72 | 8.86 | 4.95 |
| North Central | 681 | 4.35 | 1.23 | 55.87 | 4.10 | 5.94 | 3.16 | -1.99 | 1.52 | 8.00 | 3.91 |
| North East | 372 | 4.49 | 1.26 | 55.68 | 4.09 | 5.47 | 2.84 | -1.79 | 1.39 | 7.33 | 3.37 |
| North West | 41 | 4.44 | 1.30 | 56.24 | 4.21 | 4.78 | 2.90 | -2.11 | 1.11 | 6.94 | 3.20 |
| South Central | 56 | 4.33 | 1.24 | 55.11 | 4.24 | 5.72 | 3.87 | -2.14 | 1.69 | 7.92 | 4.84 |
| South East | 16 | 3.56 | 0.88 | 55.55 | 4.90 | 6.06 | 4.72 | -3.17 | 1.35 | 9.28 | 5.50 |
| West Central | 6 | 4.29 | 0.89 | 55.48 | 6.64 | 5.70 | 3.35 | -2.06 | 1.12 | 7.76 | 3.95 |
| Averagec[d] | 1423 | 4.36 | 1.22 | 55.71 | 4.11 | 5.77 | 3.22 | -1.99 | 1.50 | 7.82 | 3.94 |

[a]MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.16. Year Dough Quality Trait Average and Standard Deviations over Analysis Varieties and Production Environments.

| | | ABS[a] (%) | | EPT (minutes) | | EPV (%) | | ELS (%) | | ERS (%) | | MSE (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD | Average | SD |
| 2008 | 19 | 64.82 | 1.95 | 3.21 | 0.72 | 74.72 | 7.64 | 23.39 | 14.80 | -12.33 | 4.83 | 35.72 | 16.14 |
| 2009 | 348 | 64.73 | 1.76 | 2.84 | 0.93 | 76.32 | 5.01 | 22.94 | 14.65 | -11.90 | 3.30 | 34.85 | 15.42 |
| 2010 | 252 | 64.86 | 1.82 | 2.84 | 0.96 | 77.26 | 4.80 | 22.05 | 14.36 | -11.80 | 2.98 | 33.85 | 14.65 |
| 2011 | 163 | 65.44 | 1.50 | 3.80 | 1.24 | 74.76 | 4.13 | 23.46 | 12.24 | -11.12 | 3.06 | 34.59 | 12.00 |
| 2012 | 402 | 65.13 | 1.67 | 4.29 | 1.13 | 75.01 | 4.38 | 23.53 | 10.21 | -11.40 | 3.15 | 34.93 | 10.65 |
| 2013 | 199 | 64.74 | 1.70 | 4.28 | 0.91 | 72.02 | 4.46 | 22.60 | 9.15 | -10.75 | 2.92 | 33.34 | 9.69 |
| 2015 | 40 | 63.45 | 1.60 | 3.59 | 0.71 | 71.59 | 4.52 | 23.15 | 9.14 | -11.56 | 3.23 | 34.71 | 9.44 |
| Average[d] | 1423 | 64.91 | 1.74 | 3.59 | 1.22 | 75.18 | 4.95 | 22.97 | 12.34 | -11.49 | 3.17 | 34.46 | 12.79 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.17. Year Dough Quality Trait Average and Standard Deviations over Analysis Varieties and Production Environments (con't).

| | | MPT[a] (minutes) | | MPV (%) | | MLS (%) | | MRS (%) | | MSM (%) | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Average | SD[c] | Average | SD | Average | SD | Average | SD | Average | SD |
| 2008 | 19 | 4.01 | 1.06 | 55.62 | 6.09 | 5.81 | 3.19 | -2.29 | 1.22 | 8.13 | 3.90 |
| 2009 | 348 | 3.63 | 0.92 | 56.95 | 4.01 | 6.58 | 3.61 | -2.59 | 1.63 | 9.21 | 4.48 |
| 2010 | 252 | 3.56 | 0.94 | 57.95 | 3.85 | 7.32 | 3.45 | -2.83 | 1.65 | 10.20 | 4.30 |
| 2011 | 163 | 4.63 | 1.22 | 54.85 | 3.28 | 5.37 | 2.85 | -1.59 | 1.32 | 7.02 | 3.33 |
| 2012 | 402 | 5.05 | 1.16 | 55.01 | 3.79 | 4.90 | 2.67 | -1.39 | 1.14 | 6.40 | 2.78 |
| 2013 | 199 | 5.07 | 0.87 | 53.51 | 3.47 | 4.61 | 2.43 | -1.52 | 1.02 | 6.20 | 2.62 |
| 2015 | 40 | 4.53 | 0.67 | 52.38 | 4.13 | 4.95 | 2.57 | -1.39 | 0.82 | 6.39 | 2.80 |
| Average[d] | 1423 | 4.36 | 1.22 | 55.71 | 4.11 | 5.77 | 3.22 | -1.99 | 1.50 | 7.82 | 3.94 |

[a]MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.
[b]N:Sample Size; [c]SD: Standard Deviation. [d]Average: Population Mean.

Table 2.18. Shapiro-Wilk Test[a] for Normal Distribution for all traits.

| Trait[b] | Shapiro-Wilk |
|---|---|
| GPC | 1** |
| TWT | 0.96** |
| TKW | 1** |
| ASH | 0.98** |
| ABS | 0.99** |
| FPC | 0.99** |
| EXT | 1 |
| GI | 0.8** |
| WGC | 1** |
| DGC | 0.97** |
| WB | 1 |
| ELS | 0.91** |
| EPT | 0.98** |
| EPV | 1 |
| ERS | 0.94** |
| MLS | 0.97** |
| MPT | 0.98** |
| MPV | 1 |
| MRS | 0.97** |
| MSE | 0.92** |
| MSM | 0.94** |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight; EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding; ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 2.19. Variety Kernel Quality Data Distribution over Analysis Years and Production Environments.

| | GPC[a] (12% moisture basis) | | | | TWT (kg/hl) | | | | TKW (grams) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| ADVANCE | 68 | 5.70 | -0.18 | 1.38 | 68 | 7.49 | -0.11 | -0.98 | 68 | 15.00 | -0.32 | -0.25 |
| BARLOW | 89 | 5.00 | 0.07 | -0.18 | 89 | 10.85 | -0.83 | 1.08 | 89 | 18.50 | 0.01 | 0.91 |
| BRICK | 209 | 6.10 | -0.13 | -0.33 | 209 | 14.47 | -1.30 | 3.03 | 209 | 19.30 | -0.01 | -0.62 |
| BRIGGS | 287 | 6.70 | -0.30 | 0.47 | 287 | 14.34 | -1.03 | 1.90 | 287 | 17.40 | -0.64 | -0.24 |
| FALLER | 106 | 5.00 | -0.10 | -0.21 | 106 | 12.79 | -0.45 | 0.63 | 106 | 23.20 | 0.99 | 0.46 |
| FOREFRONT | 44 | 5.30 | 0.07 | -0.13 | 44 | 11.63 | -1.07 | 1.27 | 44 | 14.00 | -0.98 | 1.49 |
| HOWARD | 43 | 5.30 | -0.31 | -0.68 | 43 | 8.27 | -0.52 | -0.38 | 43 | 16.10 | -0.38 | 0.03 |
| PROSPER | 38 | 6.00 | 0.12 | -0.32 | 38 | 10.59 | -0.59 | 0.45 | 38 | 15.50 | 1.02 | 0.74 |
| RB07 | 208 | 5.70 | 0.23 | 0.37 | 208 | 14.47 | -0.96 | 1.26 | 208 | 19.00 | -0.47 | -0.86 |
| SELECT | 162 | 6.30 | -0.20 | -0.33 | 162 | 16.15 | -0.95 | 0.97 | 162 | 21.20 | 0.17 | 0.16 |
| STEELE-ND | 40 | 4.20 | 0.71 | -0.12 | 40 | 10.98 | -1.48 | 2.92 | 40 | 15.50 | -1.58 | 2.94 |
| TRAVERSE | 129 | 5.90 | -0.27 | 0.02 | 129 | 13.95 | -0.62 | 0.86 | 129 | 15.80 | -0.79 | 0.74 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

[b]N: Sample Size.

Table 2.20. County Kernel Quality Data Distribution over Analysis Years and Varieties.

| | GPC[a] (12% moisture basis) | | | | TWT (kg/hl) | | | | TKW (grams) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Beadle | 4 | 1.20 | -0.75 | 0.34 | 4 | 12.66 | -1.39 | 2.09 | 4 | 8.50 | 0.29 | -3.70 |
| Brookings | 71 | 6.10 | -0.08 | -0.53 | 71 | 12.92 | -0.33 | 0.29 | 71 | 18.40 | -0.49 | -0.29 |
| Brown | 157 | 5.30 | 0.10 | -0.27 | 157 | 11.89 | -0.28 | -0.69 | 157 | 18.50 | 0.33 | -0.17 |
| Campbell | 18 | 2.40 | -1.08 | 0.09 | 18 | 6.07 | 0.41 | -0.97 | 18 | 12.70 | 1.21 | 0.39 |
| Charles Mix | 12 | 4.00 | -0.37 | -0.93 | 12 | 8.91 | 0.07 | -0.88 | 12 | 5.80 | -0.49 | 0.00 |
| Clark | 41 | 7.40 | -0.51 | 2.02 | 41 | 10.72 | -0.42 | -0.59 | 41 | 15.80 | -0.19 | -0.97 |
| Codington | 24 | 4.00 | -0.02 | -0.99 | 24 | 9.95 | -0.91 | 0.10 | 24 | 16.90 | -0.43 | -1.08 |
| Corson | 30 | 5.70 | -0.47 | -0.53 | 30 | 7.75 | -0.56 | -0.51 | 30 | 16.50 | 0.41 | -0.30 |
| Day | 226 | 5.50 | -0.61 | 0.52 | 226 | 13.18 | -0.98 | 1.05 | 226 | 23.50 | 0.04 | 0.02 |
| Deuel | 16 | 4.60 | 1.39 | 2.56 | 16 | 10.21 | -0.11 | -0.85 | 16 | 9.80 | -0.39 | -0.48 |
| Dewey | 11 | 4.50 | 0.41 | -0.92 | 11 | 7.62 | -0.08 | -1.50 | 11 | 14.60 | -0.31 | -1.24 |
| Douglas | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Edmunds | 45 | 3.30 | -0.74 | -0.49 | 45 | 10.85 | -0.13 | 1.53 | 45 | 16.80 | -0.33 | 0.02 |
| Faulk | 57 | 5.50 | -0.68 | 1.72 | 57 | 14.21 | -1.25 | 1.70 | 57 | 17.30 | -0.66 | 0.35 |
| Grant | 14 | 2.40 | -0.01 | -1.63 | 14 | 10.08 | -1.35 | 1.55 | 14 | 18.30 | 0.13 | -0.40 |
| Hamlin | 7 | 1.90 | 1.67 | 3.62 | 7 | 3.36 | 0.32 | -2.49 | 7 | 4.10 | -0.40 | -2.36 |
| Hand | 85 | 4.70 | -0.23 | -0.81 | 85 | 14.73 | -0.91 | 0.87 | 85 | 16.20 | 0.09 | -0.33 |
| Hanson | 2 | 2.10 | - | - | 2 | 12.02 | - | - | 2 | 7.20 | - | - |
| Hughes | 7 | 3.10 | 2.07 | 4.68 | 7 | 6.59 | 0.66 | 0.15 | 7 | 9.10 | 0.94 | -0.94 |
| Hutchinson | 3 | 0.40 | 1.73 | - | 3 | 11.76 | -1.72 | - | 3 | 4.10 | -1.73 | - |
| Hyde | 7 | 2.60 | 1.87 | 4.22 | 7 | 10.72 | -0.41 | -0.98 | 7 | 10.20 | -1.77 | 3.79 |
| Jerauld | 17 | 4.80 | -0.61 | -0.55 | 17 | 13.31 | -0.57 | -0.58 | 17 | 12.80 | -1.23 | 1.41 |
| Jones | 23 | 3.30 | 0.54 | -0.52 | 23 | 11.37 | 0.00 | -1.40 | 23 | 14.00 | -0.76 | -0.83 |
| Kingsbury | 7 | 2.50 | 1.44 | 1.54 | 7 | 13.05 | -1.20 | 2.47 | 7 | 11.50 | -0.14 | -1.90 |
| Lake | 18 | 3.30 | 0.56 | -0.19 | 18 | 11.37 | 0.23 | -0.66 | 18 | 12.70 | -1.28 | 0.90 |
| Lyman | 8 | 4.70 | -0.43 | -1.83 | 8 | 8.14 | -0.60 | -1.34 | 8 | 7.70 | -0.52 | -0.44 |
| Marshall | 16 | 3.40 | -0.25 | -0.79 | 16 | 7.88 | 0.05 | -0.70 | 16 | 5.60 | -0.61 | -0.79 |
| McPherson | 50 | 5.20 | 0.51 | 0.41 | 50 | 12.02 | -0.47 | -0.27 | 50 | 16.00 | -0.69 | -0.24 |
| Minnehaha | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Moody | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Pennington | 6 | 5.60 | -0.40 | -0.70 | 6 | 7.24 | 0.11 | -1.61 | 6 | 5.50 | -0.17 | -2.40 |
| Potter | 80 | 5.30 | -0.25 | -0.17 | 80 | 13.70 | -1.06 | 1.51 | 80 | 22.30 | -0.32 | -0.50 |
| Roberts | 28 | 3.90 | -0.85 | 0.15 | 28 | 13.70 | -2.15 | 4.92 | 28 | 16.70 | -0.42 | -0.31 |
| Sanborn | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Spink | 76 | 6.10 | 0.50 | -0.19 | 76 | 13.57 | -0.34 | -0.30 | 76 | 24.20 | -0.52 | 0.89 |
| Sully | 31 | 5.30 | -0.03 | 0.29 | 31 | 8.01 | -0.15 | -1.10 | 31 | 11.90 | 0.29 | -0.44 |
| Tripp | 24 | 4.20 | -0.62 | -0.22 | 24 | 14.47 | -0.10 | -0.47 | 24 | 13.00 | 0.46 | -0.58 |
| Walworth | 198 | 6.80 | -0.13 | 0.37 | 198 | 14.99 | -0.87 | 1.63 | 198 | 24.10 | -0.06 | -0.33 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

[b]N: Sample Size.

Table 2.21. District Kernel Quality Data Distribution over Analysis Years and Varieties.

| | GPC[a] (12% moisture basis) | | | | TWT (kg/hl) | | | | TKW (grams) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Central | 144 | 6.80 | -0.37 | 0.08 | 144 | 14.73 | -0.81 | 0.61 | 144 | 18.20 | -0.06 | -0.24 |
| East Central | 107 | 6.80 | -0.13 | -0.07 | 107 | 15.76 | -0.73 | 1.05 | 107 | 18.40 | -0.46 | -0.68 |
| North Central | 681 | 7.00 | -0.04 | 0.12 | 681 | 16.15 | -0.70 | 0.82 | 681 | 25.90 | -0.29 | 0.00 |
| North East | 372 | 7.40 | -0.37 | 0.62 | 372 | 15.50 | -0.96 | 0.88 | 372 | 24.10 | -0.13 | -0.02 |
| North West | 41 | 5.70 | -0.23 | -0.92 | 41 | 8.40 | -0.47 | -0.85 | 41 | 17.40 | 0.14 | -0.56 |
| South Central | 56 | 5.30 | -0.45 | -0.28 | 56 | 14.60 | -0.16 | -0.92 | 56 | 16.30 | -0.51 | -0.39 |
| South East | 16 | 4.00 | -0.63 | -0.61 | 16 | 14.86 | -1.39 | 2.92 | 16 | 8.90 | -0.32 | 0.71 |
| West Central | 6 | 5.60 | -0.40 | -0.70 | 6 | 7.24 | 0.11 | -1.61 | 6 | 5.50 | -0.17 | -2.40 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.
[b]N: Sample Size.

Table 2.22. Year Kernel Quality Data Distribution over Analysis Varieties and Production Environments.

| | GPC[a] (12% moisture basis) | | | | TWT (kg/hl) | | | | TKW (grams) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| 2008 | 19 | 5.70 | -1.84 | 4.65 | 19 | 6.07 | 0.03 | -0.88 | 19 | 7.40 | 0.21 | -0.93 |
| 2009 | 348 | 6.90 | -0.12 | 0.18 | 348 | 15.76 | -0.59 | 0.48 | 348 | 18.60 | -0.05 | 0.64 |
| 2010 | 252 | 7.10 | -0.20 | 0.74 | 252 | 16.15 | -1.29 | 2.37 | 252 | 22.90 | -0.15 | 0.91 |
| 2011 | 163 | 6.40 | -0.77 | 1.48 | 163 | 15.12 | -0.66 | 0.00 | 163 | 17.80 | 0.08 | -0.40 |
| 2012 | 402 | 6.50 | -0.16 | -0.09 | 402 | 15.63 | -0.73 | 0.44 | 402 | 20.60 | -0.08 | 0.10 |
| 2013 | 199 | 6.90 | 0.03 | 0.02 | 199 | 13.82 | -0.45 | -0.11 | 199 | 18.20 | -0.13 | 0.41 |
| 2015 | 40 | 4.20 | -0.15 | -0.01 | 40 | 7.24 | -0.53 | -0.05 | 40 | 13.80 | 0.56 | 0.59 |

[a]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

[b]N: Sample Size.

Table 2.23. Variety Flour Quality Data Distribution over Analysis Years and Production Environments.

| | EXT[a] (%) | | | | ASH (12% moisture basis) | | | | FPC (12% moisture basis) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| ADVANCE | 68 | 17.29 | 0.99 | 3.49 | 68 | 0.17 | 0.97 | 1.05 | 68 | 5.46 | -0.17 | 0.78 |
| BARLOW | 89 | 11.00 | -0.20 | -0.34 | 89 | 0.11 | 0.26 | 1.39 | 89 | 4.67 | 0.20 | 0.40 |
| BRICK | 209 | 14.28 | 0.10 | -0.39 | 209 | 0.17 | 0.57 | 0.40 | 209 | 5.62 | -0.14 | 0.02 |
| BRIGGS | 287 | 19.71 | -0.52 | 1.60 | 287 | 0.15 | 0.49 | 0.55 | 287 | 7.03 | -0.49 | 0.81 |
| FALLER | 106 | 16.57 | 0.30 | -0.30 | 106 | 0.15 | 0.00 | -0.60 | 106 | 4.54 | -0.09 | -0.38 |
| FOREFRONT | 44 | 8.29 | 0.20 | -0.52 | 44 | 0.12 | 0.88 | 1.44 | 44 | 5.24 | 0.26 | 0.11 |
| HOWARD | 43 | 14.14 | -0.79 | 3.01 | 43 | 0.14 | 0.19 | -0.21 | 43 | 5.71 | -0.26 | -0.63 |
| PROSPER | 38 | 15.28 | 0.53 | 2.95 | 38 | 0.18 | -0.27 | 0.91 | 38 | 6.01 | -0.14 | -0.28 |
| RB07 | 208 | 15.14 | 0.09 | -0.11 | 208 | 0.19 | 0.65 | 1.53 | 208 | 5.72 | 0.14 | 0.91 |
| SELECT | 162 | 18.57 | 0.08 | 1.04 | 162 | 0.17 | 0.51 | 0.32 | 162 | 5.93 | -0.34 | -0.26 |
| STEELE-ND | 40 | 11.43 | -0.49 | -0.03 | 40 | 0.13 | 0.81 | 0.78 | 40 | 4.29 | 0.44 | -0.21 |
| TRAVERSE | 129 | 10.43 | 0.05 | -0.39 | 129 | 0.17 | 0.42 | -0.19 | 129 | 5.83 | -0.30 | 0.00 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content.

[b]N: Sample Size.

Table 2.24. County Flour Quality Data Distribution over Analysis Years and Varieties.

| | EXT[a] (%) | | | | ASH (14% moisture basis) | | | | FPC (14% moisture basis) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Beadle | 4 | 11.86 | 1.41 | 1.56 | 4 | 0.05 | -1.19 | 1.50 | 4 | 0.82 | -0.01 | -5.96 |
| Brookings | 71 | 12.57 | -0.11 | -0.45 | 71 | 0.20 | 0.90 | 1.30 | 71 | 5.08 | -0.32 | -0.81 |
| Brown | 157 | 15.29 | 0.33 | -0.33 | 157 | 0.15 | 0.77 | -0.11 | 157 | 5.27 | 0.03 | 0.12 |
| Campbell | 18 | 9.85 | -0.07 | 0.61 | 18 | 0.10 | -0.60 | 0.14 | 18 | 2.40 | -0.84 | 0.95 |
| Charles Mix | 12 | 8.86 | -0.46 | -0.42 | 12 | 0.15 | 0.09 | -0.49 | 12 | 4.45 | -0.24 | -1.08 |
| Clark | 41 | 15.29 | -0.70 | 0.37 | 41 | 0.13 | 0.72 | 0.47 | 41 | 6.54 | -0.87 | 2.29 |
| Codington | 24 | 13.72 | -0.48 | -0.09 | 24 | 0.13 | 0.39 | 0.23 | 24 | 3.57 | -0.11 | -1.12 |
| Corson | 30 | 11.28 | 0.28 | -0.46 | 30 | 0.19 | 1.41 | 2.81 | 30 | 5.39 | -0.57 | -0.10 |
| Day | 226 | 20.00 | -0.27 | 1.14 | 226 | 0.20 | 0.63 | 0.53 | 226 | 5.53 | -0.67 | 0.51 |
| Deuel | 16 | 8.43 | -0.82 | -0.52 | 16 | 0.11 | 0.92 | 0.81 | 16 | 4.32 | 1.06 | 1.48 |
| Dewey | 11 | 8.58 | -0.12 | -1.88 | 11 | 0.15 | -0.01 | -0.15 | 11 | 4.48 | 0.38 | -0.34 |
| Douglas | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Edmunds | 45 | 13.28 | 0.46 | -0.01 | 45 | 0.11 | -0.15 | -0.62 | 45 | 3.94 | -0.67 | -0.03 |
| Faulk | 57 | 13.29 | -0.49 | 0.42 | 57 | 0.16 | 0.58 | -0.19 | 57 | 5.48 | -0.73 | 1.71 |
| Grant | 14 | 11.57 | -0.53 | -0.42 | 14 | 0.10 | 0.34 | 0.54 | 14 | 2.26 | -0.09 | -1.35 |
| Hamlin | 7 | 8.15 | -1.18 | 0.05 | 7 | 0.14 | 0.71 | -0.82 | 7 | 1.88 | 1.90 | 4.30 |
| Hand | 85 | 18.71 | -0.17 | 0.63 | 85 | 0.16 | 0.16 | -0.37 | 85 | 5.04 | -0.24 | -0.48 |
| Hanson | 2 | 9.28 | - | - | 2 | 0.03 | - | - | 2 | 0.60 | - | - |
| Hughes | 7 | 10.00 | 0.29 | -0.40 | 7 | 0.03 | -0.77 | 0.26 | 7 | 3.96 | 1.54 | 3.18 |
| Hutchinson | 3 | 6.43 | 0.59 | - | 3 | 0.02 | 0.00 | - | 3 | 0.45 | 1.65 | - |
| Hyde | 7 | 8.14 | 0.55 | 0.93 | 7 | 0.11 | 0.81 | 1.06 | 7 | 2.51 | 1.31 | 2.62 |
| Jerauld | 17 | 12.14 | 0.44 | 0.28 | 17 | 0.10 | -0.25 | -0.84 | 17 | 4.40 | -1.06 | 0.35 |
| Jones | 23 | 9.85 | 0.73 | 0.52 | 23 | 0.11 | 0.41 | -1.14 | 23 | 3.79 | 0.87 | 0.33 |
| Kingsbury | 7 | 6.71 | -0.96 | -0.82 | 7 | 0.08 | 1.00 | -0.85 | 7 | 2.42 | 1.42 | 1.67 |
| Lake | 18 | 12.43 | -0.79 | 2.33 | 18 | 0.10 | 0.27 | 0.22 | 18 | 3.54 | 0.40 | -0.53 |
| Lyman | 8 | 8.14 | 0.33 | -1.81 | 8 | 0.11 | 0.48 | -0.38 | 8 | 5.21 | -0.41 | -1.74 |
| Marshall | 16 | 8.00 | -0.41 | 0.20 | 16 | 0.05 | -0.56 | -0.59 | 16 | 3.58 | -0.09 | -1.34 |
| McPherson | 50 | 11.43 | 0.30 | -0.12 | 50 | 0.15 | 1.20 | 1.61 | 50 | 5.10 | 0.41 | 1.42 |
| Minnehaha | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Moody | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Pennington | 6 | 4.72 | 0.17 | -0.56 | 6 | 0.11 | -0.16 | -0.54 | 6 | 6.01 | -0.39 | -0.68 |
| Potter | 80 | 15.00 | 0.05 | 0.00 | 80 | 0.15 | 0.11 | -0.74 | 80 | 5.45 | -0.43 | 0.18 |
| Roberts | 28 | 13.72 | -0.19 | -0.07 | 28 | 0.10 | 0.49 | -1.23 | 28 | 4.01 | -0.76 | 0.73 |
| Sanborn | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Spink | 76 | 16.57 | -0.01 | 0.29 | 76 | 0.17 | 0.18 | -0.28 | 76 | 6.25 | 0.13 | -0.57 |
| Sully | 31 | 13.72 | -0.02 | -0.29 | 31 | 0.11 | 0.14 | -1.16 | 31 | 4.92 | -0.01 | 0.21 |
| Tripp | 24 | 9.86 | -0.48 | -0.23 | 24 | 0.16 | 0.49 | -0.70 | 24 | 4.72 | -0.60 | -0.17 |
| Walworth | 198 | 16.00 | 0.23 | 0.15 | 198 | 0.20 | 0.58 | 0.41 | 198 | 6.43 | -0.14 | 0.41 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content.

[b]N: Sample Size.

Table 2.25. District Flour Quality Data Distribution over Analysis Years and Varieties.

| | EXT[a] (%) | | | | ASH (14% moisture basis) | | | | FPC (14% moisture basis) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Central | 144 | 21.14 | 0.15 | 0.58 | 144 | 0.16 | 0.08 | -0.69 | 144 | 6.79 | -0.47 | 0.99 |
| East Central | 107 | 14.28 | -0.16 | -0.23 | 107 | 0.20 | 0.65 | 1.10 | 107 | 6.93 | -0.25 | -0.04 |
| North Central | 681 | 16.85 | 0.15 | -0.07 | 681 | 0.20 | 0.51 | 0.15 | 681 | 6.93 | -0.16 | 0.27 |
| North East | 372 | 20.00 | -0.48 | 0.75 | 372 | 0.20 | 0.69 | 0.59 | 372 | 6.54 | -0.46 | 0.44 |
| North West | 41 | 13.43 | -0.01 | -0.44 | 41 | 0.20 | 0.95 | 1.14 | 41 | 5.39 | -0.31 | -0.57 |
| South Central | 56 | 11.28 | 0.18 | -0.63 | 56 | 0.16 | 0.47 | -0.60 | 56 | 5.51 | -0.37 | -0.24 |
| South East | 16 | 8.86 | -0.41 | -0.90 | 16 | 0.17 | -0.47 | -0.15 | 16 | 4.45 | -0.47 | -0.71 |
| West Central | 6 | 4.72 | 0.17 | -0.56 | 6 | 0.11 | -0.16 | -0.54 | 6 | 6.01 | -0.39 | -0.68 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content.

[b]N: Sample Size.

Table 2.26. Year Flour Quality Data Distribution over Analysis Varieties and Production Environments.

| | EXT[a] (%) | | | | ASH (14% moisture basis) | | | | FPC (14% moisture basis) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| 2008 | 19 | 8.85 | 1.31 | 1.44 | 19 | 0.08 | 0.53 | -0.92 | 19 | 5.54 | -1.69 | 3.93 |
| 2009 | 348 | 14.28 | 0.04 | -0.22 | 348 | 0.20 | 0.89 | 1.34 | 348 | 6.82 | -0.10 | 0.01 |
| 2010 | 252 | 15.14 | -0.17 | 0.54 | 252 | 0.20 | 0.68 | 0.64 | 252 | 7.13 | -0.34 | 0.90 |
| 2011 | 163 | 17.14 | -0.06 | 0.89 | 163 | 0.21 | 0.55 | 0.99 | 163 | 6.30 | -0.86 | 1.90 |
| 2012 | 402 | 19.85 | -0.03 | 0.98 | 402 | 0.19 | 0.27 | -0.13 | 402 | 6.50 | -0.26 | 0.08 |
| 2013 | 199 | 18.86 | 0.41 | 1.05 | 199 | 0.23 | 0.27 | -0.21 | 199 | 6.53 | -0.04 | 0.08 |
| 2015 | 40 | 9.57 | -0.68 | 0.60 | 40 | 0.14 | -0.07 | -0.37 | 40 | 4.44 | -0.33 | -0.08 |

[a]EXT: flour extraction; ASH: ash content; FPC: flour protein content.

[b]N: Sample Size.

Table 2.27. Variety Flour Quality Data Distribution over Analysis Years and Production Environments.

| | GI[a] | | | | WGC(%) | | | | DGC(%) | | | | WB(%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| ADVANCE | 68 | 15.15 | -4.27 | 21.89 | 68 | 14.86 | 0.21 | 0.35 | 68 | 5.43 | 0.25 | 0.50 | 68 | 9.55 | 0.21 | 0.25 |
| BARLOW | 89 | 19.67 | -1.16 | 1.46 | 89 | 15.85 | 0.05 | 0.36 | 89 | 8.31 | 1.20 | 5.06 | 89 | 10.60 | 0.07 | 0.38 |
| BRICK | 209 | 22.65 | -4.01 | 21.68 | 209 | 26.11 | 0.52 | 1.78 | 209 | 11.78 | 1.16 | 5.37 | 209 | 14.33 | 0.24 | 0.61 |
| BRIGGS | 287 | 37.40 | -0.28 | -0.62 | 287 | 24.62 | -0.21 | 0.56 | 287 | 8.74 | -0.15 | 0.98 | 287 | 17.12 | -0.28 | 0.43 |
| FALLER | 106 | 19.66 | -1.32 | 0.98 | 106 | 15.27 | 0.12 | -0.36 | 106 | 5.03 | 0.06 | -0.37 | 106 | 10.45 | 0.14 | -0.42 |
| FOREFRONT | 44 | 13.51 | -1.55 | 2.35 | 44 | 17.30 | 0.08 | -0.14 | 44 | 6.24 | 0.41 | 0.53 | 44 | 11.16 | -0.05 | -0.33 |
| HOWARD | 43 | 27.62 | -1.08 | 0.32 | 43 | 23.60 | -0.33 | -0.21 | 43 | 8.44 | -0.24 | 0.18 | 43 | 15.20 | -0.29 | -0.38 |
| PROSPER | 38 | 36.82 | -1.93 | 3.41 | 38 | 20.20 | 0.03 | -0.50 | 38 | 7.07 | -0.18 | -0.39 | 38 | 14.44 | 0.20 | -0.61 |
| RB07 | 208 | 46.81 | -2.23 | 8.23 | 208 | 28.99 | 0.92 | 4.77 | 208 | 14.38 | 2.51 | 17.67 | 208 | 15.91 | 0.31 | 1.73 |
| SELECT | 162 | 27.94 | -1.59 | 2.24 | 162 | 18.83 | -0.24 | -0.55 | 162 | 6.37 | -0.23 | -0.42 | 162 | 12.48 | -0.14 | -0.58 |
| STEELE-ND | 40 | 23.55 | -1.56 | 1.97 | 40 | 15.37 | -0.37 | 0.79 | 40 | 6.06 | -0.02 | 0.89 | 40 | 10.53 | -0.15 | 0.47 |
| TRAVERSE | 129 | 55.29 | -0.07 | -0.76 | 129 | 25.82 | -0.42 | 0.66 | 129 | 9.39 | -0.20 | 0.77 | 129 | 17.20 | -0.42 | 0.68 |

[a]GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

[b]N: Sample Size.

Table 2.28. Variety Flour Quality Data Distribution over Analysis Years and Varieties.

| | GI[a] | | | | WGC(%) | | | | DGC(%) | | | | WB(%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Beadle | 4 | 44.93 | -1.90 | 3.68 | 4 | 7.24 | 0.35 | 0.59 | 4 | 1.33 | -1.30 | 2.06 | 4 | 5.91 | 0.66 | 0.12 |
| Brookings | 71 | 28.51 | -1.41 | 1.39 | 71 | 17.99 | 0.06 | -0.81 | 71 | 8.22 | 0.44 | 0.58 | 71 | 13.17 | 0.16 | -0.60 |
| Brown | 157 | 46.79 | -1.45 | 1.82 | 157 | 17.34 | 0.25 | -0.30 | 157 | 9.17 | 1.00 | 3.11 | 157 | 12.56 | 0.25 | -0.27 |
| Campbell | 18 | 26.96 | -0.30 | -1.50 | 18 | 8.78 | 0.17 | -0.85 | 18 | 2.37 | 0.42 | -0.08 | 18 | 6.42 | 0.11 | -1.08 |
| Charles Mix | 12 | 51.93 | -0.77 | -0.84 | 12 | 15.85 | 0.07 | -0.59 | 12 | 4.80 | -0.36 | -0.76 | 12 | 11.04 | 0.35 | -0.45 |
| Clark | 41 | 40.83 | -1.58 | 2.16 | 41 | 20.99 | -0.88 | 3.12 | 41 | 7.69 | -1.15 | 4.23 | 41 | 13.58 | -0.60 | 2.20 |
| Codington | 24 | 36.92 | -1.34 | 0.20 | 24 | 15.28 | 0.16 | -0.72 | 24 | 5.64 | 0.11 | -0.56 | 24 | 10.71 | 0.30 | -0.59 |
| Corson | 30 | 44.75 | -1.29 | 2.41 | 30 | 27.09 | 0.76 | 2.17 | 30 | 13.67 | 2.35 | 9.45 | 30 | 13.64 | -0.06 | -0.06 |
| Day | 226 | 40.04 | -1.83 | 3.02 | 226 | 20.94 | -0.39 | 0.13 | 226 | 8.19 | -0.46 | 0.34 | 226 | 14.44 | -0.23 | 0.04 |
| Deuel | 16 | 54.72 | -1.87 | 2.87 | 16 | 8.51 | 0.68 | -1.00 | 16 | 3.66 | 0.72 | 0.29 | 16 | 5.87 | 0.66 | -1.20 |
| Dewey | 11 | 32.87 | -2.02 | 4.66 | 11 | 11.93 | 1.36 | 2.84 | 11 | 4.18 | 0.19 | -0.32 | 11 | 10.27 | 0.55 | 2.63 |
| Douglas | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Edmunds | 45 | 37.15 | -0.67 | -0.44 | 45 | 14.47 | -0.32 | -0.06 | 45 | 4.38 | -0.01 | -0.05 | 45 | 10.16 | -0.29 | -0.23 |
| Faulk | 57 | 37.65 | -1.30 | 0.87 | 57 | 19.03 | -0.12 | -0.49 | 57 | 6.72 | 0.07 | 0.34 | 57 | 12.29 | -0.17 | -0.77 |
| Grant | 14 | 16.08 | -1.53 | 2.08 | 14 | 9.22 | -0.16 | -1.00 | 14 | 3.08 | -0.66 | -0.20 | 14 | 6.37 | 0.11 | -0.90 |
| Hamlin | 7 | 11.47 | -1.17 | 0.55 | 7 | 7.51 | 0.80 | 0.56 | 7 | 2.40 | 1.37 | 2.24 | 7 | 5.11 | 0.40 | -0.29 |
| Hand | 85 | 54.29 | -1.32 | 1.23 | 85 | 18.68 | -0.12 | -0.67 | 85 | 5.98 | -0.28 | -0.46 | 85 | 15.26 | -0.20 | -0.32 |
| Hanson | 2 | 2.50 | - | - | 2 | 1.60 | - | - | 2 | 0.15 | - | - | 2 | 1.46 | - | - |
| Hughes | 7 | 20.52 | -2.50 | 6.39 | 7 | 16.30 | 2.05 | 4.55 | 7 | 4.91 | 1.96 | 4.21 | 7 | 11.69 | 2.06 | 4.60 |
| Hutchinson | 3 | 41.40 | -1.73 | - | 3 | 6.21 | 1.67 | - | 3 | 0.80 | 1.72 | - | 3 | 5.44 | 1.64 | - |
| Hyde | 7 | 13.93 | -2.07 | 4.54 | 7 | 9.82 | 1.74 | 3.85 | 7 | 3.29 | 1.68 | 3.53 | 7 | 6.53 | 1.74 | 3.77 |
| Jerauld | 17 | 28.47 | -1.36 | 0.47 | 17 | 14.80 | 0.04 | -0.55 | 17 | 4.73 | -0.62 | -0.51 | 17 | 10.13 | 0.47 | -0.55 |
| Jones | 23 | 41.17 | -0.83 | -0.77 | 23 | 16.46 | 0.14 | -0.62 | 23 | 4.86 | 0.19 | -0.33 | 23 | 11.89 | 0.20 | -0.61 |
| Kingsbury | 7 | 25.32 | -1.44 | 0.78 | 7 | 9.31 | 0.01 | -1.80 | 7 | 3.70 | 0.22 | -0.28 | 7 | 5.82 | 0.07 | -2.28 |
| Lake | 18 | 52.99 | -0.38 | 0.28 | 18 | 16.43 | 1.03 | 2.71 | 18 | 5.75 | 1.79 | 4.57 | 18 | 10.68 | 0.51 | 1.59 |
| Lyman | 8 | 13.16 | 0.00 | -2.27 | 8 | 17.23 | -0.08 | -2.22 | 8 | 5.86 | -0.16 | -2.24 | 8 | 11.36 | -0.04 | -2.18 |
| Marshall | 16 | 45.76 | -0.69 | -0.18 | 16 | 11.83 | -0.65 | -0.34 | 16 | 3.88 | -0.59 | -0.62 | 16 | 7.95 | -0.57 | -0.49 |
| McPherson | 50 | 46.75 | -1.57 | 1.76 | 50 | 16.86 | 1.03 | 1.70 | 50 | 5.88 | 0.86 | 1.16 | 50 | 11.35 | 0.95 | 1.48 |
| Minnehaha | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Moody | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Pennington | 6 | 34.16 | -1.55 | 1.69 | 6 | 17.17 | -1.51 | 3.07 | 6 | 6.49 | -0.81 | 1.11 | 6 | 10.69 | -1.85 | 4.05 |
| Potter | 80 | 33.32 | -0.73 | -0.59 | 80 | 20.74 | -0.08 | 0.83 | 80 | 6.43 | -0.32 | 0.45 | 80 | 16.08 | -0.02 | 0.89 |
| Roberts | 28 | 22.03 | -1.30 | 0.92 | 28 | 12.43 | 0.88 | 0.90 | 28 | 5.02 | 0.57 | 1.48 | 28 | 7.92 | 0.85 | 0.46 |
| Sanborn | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Spink | 76 | 41.88 | -1.51 | 1.64 | 76 | 18.12 | 0.03 | -0.68 | 76 | 7.29 | 0.10 | -0.47 | 76 | 12.88 | 0.13 | -0.60 |
| Sully | 31 | 46.27 | -2.20 | 5.61 | 31 | 17.82 | 1.39 | 1.92 | 31 | 6.57 | 1.11 | 0.75 | 31 | 13.64 | 1.11 | 1.90 |
| Tripp | 24 | 43.90 | -0.73 | -0.55 | 24 | 14.01 | -0.21 | -0.39 | 24 | 4.95 | -0.22 | -0.77 | 24 | 9.88 | -0.24 | -0.32 |
| Walworth | 198 | 46.71 | -2.50 | 7.90 | 198 | 26.11 | 0.09 | 0.85 | 198 | 11.78 | 0.75 | 4.48 | 198 | 14.79 | -0.01 | 0.14 |

[a]GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

[b]N: Sample Size.

Table 2.29. District Flour Quality Data Distribution over Analysis Years and Varieties.

| | GI[a] | | | | WGC(%) | | | | DGC(%) | | | | WB(%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Central | 144 | 54.98 | -1.59 | 2.16 | 144 | 22.95 | 0.11 | -0.01 | 144 | 8.71 | 0.07 | 0.75 | 144 | 15.74 | 0.11 | -0.09 |
| East Central | 107 | 54.53 | -1.52 | 2.46 | 107 | 23.18 | 0.20 | 0.19 | 107 | 8.22 | 0.52 | 1.15 | 107 | 15.79 | 0.19 | -0.05 |
| North Central | 681 | 47.99 | -1.51 | 2.01 | 681 | 26.11 | 0.06 | 0.26 | 681 | 11.89 | 0.43 | 1.97 | 681 | 18.14 | 0.05 | 0.02 |
| North East | 372 | 55.79 | -1.97 | 4.06 | 372 | 22.47 | -0.29 | 0.28 | 372 | 9.15 | -0.39 | 0.63 | 372 | 15.01 | -0.14 | 0.11 |
| North West | 41 | 44.75 | -1.38 | 2.27 | 41 | 27.09 | 1.00 | 2.62 | 41 | 13.67 | 2.50 | 11.21 | 41 | 13.82 | 0.17 | -0.01 |
| South Central | 56 | 44.11 | -0.93 | -0.28 | 56 | 19.62 | -0.37 | -0.52 | 56 | 6.66 | -0.41 | -0.35 | 56 | 13.18 | -0.30 | -0.62 |
| South East | 16 | 54.80 | -0.77 | -0.87 | 16 | 15.85 | 0.18 | -0.56 | 16 | 4.80 | -0.52 | -0.54 | 16 | 11.04 | 0.50 | -0.50 |
| West Central | 6 | 34.16 | -1.55 | 1.69 | 6 | 17.17 | -1.51 | 3.07 | 6 | 6.49 | -0.81 | 1.11 | 6 | 10.69 | -1.85 | 4.05 |

[a]GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

[b]N: Sample Size.

Table 2.30. Year Flour Quality Data Distribution over Analysis Varieties and Production Environments.

| | GI[a] | | | | WGC(%) | | | | DGC(%) | | | | WB(%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| 2008 | 19 | 35.85 | -1.22 | 0.87 | 19 | 20.10 | -1.96 | 5.73 | 19 | 8.96 | -1.48 | 5.08 | 19 | 12.95 | -1.81 | 5.17 |
| 2009 | 348 | 54.53 | -1.04 | 0.43 | 348 | 24.62 | -0.08 | 0.12 | 348 | 8.69 | 0.10 | 0.59 | 348 | 17.25 | -0.12 | 0.15 |
| 2010 | 252 | 56.11 | -1.18 | 0.96 | 252 | 30.22 | 0.52 | 1.68 | 252 | 15.14 | 1.30 | 8.57 | 252 | 15.38 | 0.28 | 0.40 |
| 2011 | 163 | 38.17 | -1.51 | 2.40 | 163 | 17.68 | -0.71 | 0.33 | 163 | 6.74 | -0.82 | 1.05 | 163 | 11.89 | -0.55 | -0.06 |
| 2012 | 402 | 44.17 | -1.99 | 4.22 | 402 | 27.19 | 0.01 | 0.15 | 402 | 12.38 | 0.61 | 3.16 | 402 | 14.81 | 0.04 | -0.18 |
| 2013 | 199 | 37.71 | -2.48 | 6.58 | 199 | 21.47 | 0.21 | 0.00 | 199 | 7.29 | 0.05 | -0.10 | 199 | 14.29 | 0.30 | 0.13 |
| 2015 | 40 | 20.94 | -2.00 | 4.21 | 40 | 13.76 | -0.01 | -0.45 | 40 | 4.55 | -0.13 | -0.64 | 40 | 9.21 | 0.09 | -0.40 |

[a]GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

[b]N: Sample Size.

Table 2.31. Variety Dough Quality Data Distribution over Analysis Years and Production Environments.

| | ABS[a] (%) | | | | EPT (minutes) | | | | EPV (%) | | | | ELS (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| ADVANCE | 68 | 8.19 | -0.17 | 0.78 | 68 | 4.41 | -0.20 | -0.01 | 68 | 17.47 | 0.33 | -0.46 | 68 | 44.16 | 1.17 | 2.42 |
| BARLOW | 89 | 7.00 | 0.20 | 0.41 | 89 | 3.05 | -0.21 | -0.49 | 89 | 22.41 | -0.07 | 0.50 | 89 | 56.85 | 0.76 | -0.42 |
| BRICK | 209 | 8.44 | -0.14 | 0.03 | 209 | 6.34 | -0.13 | 0.05 | 209 | 32.19 | 0.10 | 0.60 | 209 | 50.10 | 1.57 | 2.46 |
| BRIGGS | 287 | 10.56 | -0.49 | 0.81 | 287 | 4.96 | 1.22 | 2.12 | 287 | 29.42 | -0.25 | 0.30 | 287 | 70.75 | 1.57 | 3.02 |
| FALLER | 106 | 6.82 | -0.09 | -0.38 | 106 | 5.84 | 0.26 | 0.83 | 106 | 24.42 | -0.03 | -0.29 | 106 | 59.61 | 0.81 | 0.31 |
| FOREFRONT | 44 | 7.86 | 0.27 | 0.12 | 44 | 5.28 | 0.10 | 0.80 | 44 | 18.49 | 0.73 | 0.72 | 44 | 41.84 | 0.71 | 0.56 |
| HOWARD | 43 | 8.56 | -0.26 | -0.63 | 43 | 3.39 | 0.48 | -0.52 | 43 | 24.75 | 0.22 | 0.40 | 43 | 63.56 | 0.99 | 0.08 |
| PROSPER | 38 | 9.00 | -0.13 | -0.28 | 38 | 4.52 | -0.31 | -0.10 | 38 | 14.86 | 0.09 | -1.15 | 38 | 73.96 | 1.52 | 4.07 |
| RB07 | 208 | 8.57 | 0.13 | 0.91 | 208 | 4.47 | 0.36 | -0.11 | 208 | 19.67 | -0.37 | -0.18 | 208 | 59.76 | 1.53 | 4.27 |
| SELECT | 162 | 8.91 | -0.34 | -0.26 | 162 | 6.39 | 0.37 | 0.82 | 162 | 25.01 | -0.02 | -0.17 | 162 | 61.62 | 0.95 | 0.50 |
| STEELE-ND | 40 | 6.44 | 0.43 | -0.21 | 40 | 2.95 | 0.39 | -0.18 | 40 | 16.30 | -0.22 | -0.29 | 40 | 56.43 | 0.74 | -0.76 |
| TRAVERSE | 129 | 8.74 | -0.30 | 0.01 | 129 | 4.38 | 1.50 | 3.61 | 129 | 32.86 | -0.46 | 0.73 | 129 | 70.07 | 1.12 | 0.97 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope.

[b]N: Sample Size.

Table 2.32. Variety Dough Quality Data Distribution over Analysis Years and Varieties.

| | ABS[a] (%) | | | | EPT (minutes) | | | | EPV (%) | | | | ELS (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Beadle | 4 | 1.24 | -0.01 | -5.96 | 4 | 1.78 | 0.01 | -5.79 | 4 | 15.76 | -1.59 | 2.35 | 4 | 25.04 | -0.90 | 1.40 |
| Brookings | 71 | 7.62 | -0.32 | -0.82 | 71 | 6.31 | 0.66 | 0.76 | 71 | 23.56 | -0.44 | 0.43 | 71 | 62.31 | 1.13 | 1.18 |
| Brown | 157 | 7.89 | 0.03 | 0.11 | 157 | 5.31 | 0.18 | -0.56 | 157 | 20.06 | 0.20 | -0.30 | 157 | 65.04 | 0.74 | 0.74 |
| Campbell | 18 | 3.60 | -0.84 | 0.96 | 18 | 3.43 | 0.10 | -1.19 | 18 | 11.92 | -0.53 | -0.94 | 18 | 42.02 | 0.20 | 0.13 |
| Charles Mix | 12 | 6.68 | -0.23 | -1.08 | 12 | 1.69 | -0.20 | -1.20 | 12 | 23.51 | -0.24 | -1.02 | 12 | 65.56 | 0.38 | -1.50 |
| Clark | 41 | 9.81 | -0.87 | 2.29 | 41 | 6.15 | 0.60 | -0.24 | 41 | 31.06 | -1.39 | 4.29 | 41 | 69.54 | 1.57 | 3.35 |
| Codington | 24 | 5.36 | -0.11 | -1.12 | 24 | 5.03 | 0.05 | -0.94 | 24 | 13.32 | -0.12 | -1.44 | 24 | 40.78 | -0.10 | -0.25 |
| Corson | 30 | 8.09 | -0.57 | -0.10 | 30 | 5.65 | 1.02 | 0.84 | 30 | 17.58 | -0.34 | -0.93 | 30 | 60.98 | 1.30 | 1.57 |
| Day | 226 | 8.29 | -0.67 | 0.51 | 226 | 5.59 | 0.26 | -0.55 | 226 | 27.34 | -0.04 | -0.06 | 226 | 57.77 | 1.11 | 0.94 |
| Deuel | 16 | 6.48 | 1.06 | 1.47 | 16 | 2.99 | -0.29 | -1.35 | 16 | 16.76 | 0.02 | -0.97 | 16 | 34.38 | -0.53 | -0.17 |
| Dewey | 11 | 6.72 | 0.38 | -0.34 | 11 | 3.92 | 0.59 | -0.03 | 11 | 16.08 | 0.88 | -0.15 | 11 | 53.24 | 1.34 | 2.50 |
| Douglas | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Edmunds | 45 | 5.90 | -0.67 | -0.03 | 45 | 4.52 | 0.31 | -0.90 | 45 | 20.54 | -0.27 | 0.20 | 45 | 46.88 | 1.15 | 0.59 |
| Faulk | 57 | 8.23 | -0.73 | 1.71 | 57 | 5.60 | 0.56 | 0.19 | 57 | 20.17 | 0.67 | 0.41 | 57 | 67.26 | 1.00 | 1.05 |
| Grant | 14 | 3.39 | -0.10 | -1.34 | 14 | 3.38 | 1.59 | 3.26 | 14 | 13.14 | -0.76 | -0.43 | 14 | 39.38 | 1.00 | 0.01 |
| Hamlin | 7 | 2.81 | 1.91 | 4.31 | 7 | 2.03 | 1.43 | 1.73 | 7 | 10.54 | -0.70 | -0.46 | 7 | 24.59 | 1.13 | 0.30 |
| Hand | 85 | 7.55 | -0.24 | -0.48 | 85 | 4.84 | 0.33 | 0.02 | 85 | 19.82 | -0.15 | -0.54 | 85 | 60.28 | 1.21 | 1.87 |
| Hanson | 2 | 0.89 | - | - | 2 | 0.87 | - | - | 2 | 0.30 | - | - | 2 | 19.83 | - | - |
| Hughes | 7 | 5.93 | 1.54 | 3.16 | 7 | 3.20 | -0.51 | 0.42 | 7 | 11.52 | 1.50 | 3.10 | 7 | 17.13 | 0.10 | -0.30 |
| Hutchinson | 3 | 0.69 | 1.64 | - | 3 | 2.05 | 0.97 | - | 3 | 15.93 | -1.62 | - | 3 | 6.53 | 0.46 | - |
| Hyde | 7 | 3.76 | 1.32 | 2.62 | 7 | 2.64 | -0.10 | -1.31 | 7 | 9.45 | 0.01 | -0.91 | 7 | 7.59 | 0.63 | -1.38 |
| Jerauld | 17 | 6.60 | -1.06 | 0.35 | 17 | 3.12 | -0.31 | -0.80 | 17 | 11.84 | 0.65 | -0.58 | 17 | 41.01 | 0.98 | -0.51 |
| Jones | 23 | 5.69 | 0.87 | 0.33 | 23 | 4.78 | 0.17 | -1.10 | 23 | 18.25 | 0.07 | 1.70 | 23 | 60.93 | 1.46 | 3.00 |
| Kingsbury | 7 | 3.62 | 1.43 | 1.69 | 7 | 2.80 | -0.45 | -2.18 | 7 | 8.24 | -0.43 | 0.06 | 7 | 55.19 | 0.53 | -0.12 |
| Lake | 18 | 5.31 | 0.40 | -0.52 | 18 | 3.20 | 0.96 | 0.95 | 18 | 13.44 | 0.42 | -0.87 | 18 | 61.69 | 0.56 | -0.89 |
| Lyman | 8 | 7.83 | -0.41 | -1.74 | 8 | 3.16 | 0.00 | -2.03 | 8 | 19.45 | -0.41 | -1.34 | 8 | 21.89 | 0.68 | 2.73 |
| Marshall | 16 | 5.37 | -0.08 | -1.34 | 16 | 3.57 | 0.42 | -1.29 | 16 | 18.41 | 0.15 | -0.98 | 16 | 49.35 | 1.63 | 1.75 |
| McPherson | 50 | 7.65 | 0.41 | 1.42 | 50 | 4.21 | 0.55 | 0.56 | 50 | 22.45 | 0.58 | 0.94 | 50 | 64.56 | 1.31 | 1.20 |
| Minnehaha | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Moody | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Pennington | 6 | 9.02 | -0.39 | -0.68 | 6 | 1.51 | 0.97 | 0.57 | 6 | 22.29 | -0.84 | -0.30 | 6 | 47.34 | -0.01 | -1.88 |
| Potter | 80 | 8.19 | -0.42 | 0.18 | 80 | 6.50 | 0.87 | 1.10 | 80 | 23.05 | -0.19 | -0.08 | 80 | 74.03 | 1.74 | 4.54 |
| Roberts | 28 | 6.02 | -0.76 | 0.74 | 28 | 5.19 | 0.51 | -0.90 | 28 | 19.13 | -0.62 | 0.97 | 28 | 59.01 | 1.96 | 5.44 |
| Sanborn | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Spink | 76 | 9.37 | 0.13 | -0.58 | 76 | 5.65 | 0.55 | -0.17 | 76 | 26.02 | -0.12 | -0.47 | 76 | 56.00 | 1.07 | 0.83 |
| Sully | 31 | 7.38 | -0.01 | 0.21 | 31 | 4.14 | 0.05 | -1.17 | 31 | 20.54 | -0.01 | -0.65 | 31 | 39.55 | 1.20 | 1.91 |
| Tripp | 24 | 7.07 | -0.60 | -0.17 | 24 | 4.00 | 0.17 | -1.07 | 24 | 21.53 | -0.51 | -0.34 | 24 | 46.18 | 0.59 | 1.07 |
| Walworth | 198 | 9.63 | -0.14 | 0.41 | 198 | 5.45 | 0.26 | -0.65 | 198 | 28.09 | 0.10 | -0.22 | 198 | 67.74 | 1.78 | 3.74 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope.

[b]N: Sample Size.

Table 2.33. District Dough Quality Data Distribution over Analysis Years and Varieties.

| | ABS[a] (%) | | | | EPT (minutes) | | | | EPV (%) | | | | ELS (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Central | 144 | 10.18 | -0.47 | 0.99 | 144 | 4.84 | 0.25 | -0.51 | 144 | 27.74 | -0.05 | -0.22 | 144 | 60.28 | 1.22 | 1.72 |
| East Central | 107 | 10.39 | -0.25 | -0.04 | 107 | 6.31 | 0.60 | 0.25 | 107 | 23.56 | -0.23 | 0.42 | 107 | 63.56 | 1.05 | 0.74 |
| North Central | 681 | 10.40 | -0.16 | 0.27 | 681 | 6.76 | 0.45 | -0.19 | 681 | 31.23 | 0.04 | 0.13 | 681 | 74.25 | 1.27 | 2.01 |
| North East | 372 | 9.81 | -0.46 | 0.44 | 372 | 6.20 | 0.42 | -0.31 | 372 | 37.25 | -0.29 | 0.76 | 372 | 70.95 | 1.22 | 2.00 |
| North West | 41 | 8.09 | -0.31 | -0.56 | 41 | 5.65 | 0.91 | 0.59 | 41 | 21.80 | 0.00 | -0.72 | 41 | 62.91 | 1.26 | 1.45 |
| South Central | 56 | 8.28 | -0.38 | -0.24 | 56 | 4.85 | 0.21 | -0.97 | 56 | 22.57 | -0.49 | 0.09 | 56 | 60.93 | 1.17 | 2.89 |
| South East | 16 | 6.68 | -0.47 | -0.71 | 16 | 2.35 | 0.35 | -0.02 | 16 | 23.51 | -0.09 | -1.24 | 16 | 65.56 | 0.79 | -0.73 |
| West Central | 6 | 9.02 | -0.39 | -0.68 | 6 | 1.51 | 0.97 | 0.57 | 6 | 22.29 | -0.84 | -0.30 | 6 | 47.34 | -0.01 | -1.88 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope.

[b]N: Sample Size.

Table 2.34. Year Dough Quality Data Distribution over Analysis Varieties and Production Environments.

| | ABS[a] (%) | | | | EPT (minutes) | | | | EPV (%) | | | | ELS (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| 2008 | 19 | 8.31 | -1.70 | 3.94 | 19 | 2.35 | 0.39 | -0.67 | 19 | 35.50 | -1.03 | 2.96 | 19 | 58.86 | 1.72 | 3.48 |
| 2009 | 348 | 10.24 | -0.10 | 0.01 | 348 | 4.98 | 0.86 | 0.57 | 348 | 28.80 | -0.22 | 0.05 | 348 | 70.95 | 1.23 | 1.34 |
| 2010 | 252 | 10.68 | -0.34 | 0.89 | 252 | 4.78 | 0.79 | 0.07 | 252 | 29.95 | -0.58 | 0.99 | 252 | 65.67 | 1.11 | 1.02 |
| 2011 | 163 | 9.45 | -0.86 | 1.90 | 163 | 5.44 | 0.40 | -0.32 | 163 | 23.84 | -0.02 | 0.29 | 163 | 64.99 | 1.16 | 1.39 |
| 2012 | 402 | 9.75 | -0.26 | 0.08 | 402 | 6.25 | 0.51 | 0.17 | 402 | 27.75 | 0.10 | 0.26 | 402 | 69.45 | 1.31 | 2.02 |
| 2013 | 199 | 9.79 | -0.04 | 0.08 | 199 | 5.16 | 0.06 | -0.16 | 199 | 23.97 | 0.14 | -0.13 | 199 | 43.76 | 1.15 | 0.93 |
| 2015 | 40 | 6.67 | -0.34 | -0.08 | 40 | 3.69 | 0.04 | 0.82 | 40 | 19.07 | -0.35 | 0.28 | 40 | 38.05 | 1.04 | 0.86 |

[a]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope.

[b]N: Sample Size.

Table 2.35. Variety Dough Quality Data Distribution over Analysis Years and Production Environments.

| | ERS[a] (%) | | | | MSE (%) | | | | MPT (minutes) | | | | MPV (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| ADVANCE | 68 | 11.53 | -0.42 | -0.30 | 68 | 43.14 | 0.96 | 1.24 | 68 | 4.03 | -0.15 | 0.02 | 68 | 15.49 | 0.05 | -0.18 |
| BARLOW | 89 | 12.84 | -0.73 | 0.76 | 89 | 61.36 | 0.73 | -0.28 | 89 | 3.07 | 0.08 | -0.35 | 89 | 16.52 | -0.04 | -0.63 |
| BRICK | 209 | 18.24 | -0.79 | 0.78 | 209 | 58.76 | 1.43 | 2.45 | 209 | 6.85 | 0.05 | -0.07 | 209 | 25.30 | 0.73 | 1.33 |
| BRIGGS | 287 | 16.49 | -0.88 | 1.19 | 287 | 76.30 | 1.51 | 2.78 | 287 | 4.82 | 1.35 | 2.92 | 287 | 28.78 | 0.09 | 0.59 |
| FALLER | 106 | 14.03 | -0.76 | 0.41 | 106 | 54.32 | 0.68 | -0.17 | 106 | 6.48 | 0.61 | 2.18 | 106 | 15.81 | -0.20 | -0.53 |
| FOREFRONT | 44 | 12.98 | -0.87 | 0.35 | 44 | 42.05 | 1.01 | 0.69 | 44 | 4.70 | -0.18 | 1.48 | 44 | 13.48 | 0.45 | -0.23 |
| HOWARD | 43 | 12.36 | -0.83 | 0.39 | 43 | 66.24 | 0.98 | 0.21 | 43 | 3.10 | 0.16 | -0.42 | 43 | 21.60 | 0.05 | 0.32 |
| PROSPER | 38 | 22.16 | -1.93 | 3.82 | 38 | 68.96 | 1.26 | 2.45 | 38 | 3.97 | -0.58 | -0.12 | 38 | 15.95 | -0.25 | -0.38 |
| RB07 | 208 | 17.60 | -1.18 | 2.29 | 208 | 61.72 | 1.55 | 4.62 | 208 | 5.46 | 0.74 | 1.16 | 208 | 21.55 | -0.11 | 0.01 |
| SELECT | 162 | 13.44 | -0.47 | -0.55 | 162 | 69.10 | 0.99 | 0.88 | 162 | 5.92 | 0.18 | 1.10 | 162 | 18.50 | 0.03 | -0.38 |
| STEELE-ND | 40 | 13.26 | -1.12 | 2.23 | 40 | 59.51 | 0.75 | -0.65 | 40 | 3.13 | 0.70 | 1.04 | 40 | 16.06 | 0.08 | -0.33 |
| TRAVERSE | 129 | 21.44 | -0.90 | 1.61 | 129 | 76.94 | 1.10 | 0.83 | 129 | 6.00 | 2.02 | 7.15 | 129 | 25.89 | -0.25 | 0.44 |

[a]ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value.

[b]N: Sample Size.

Table 2.36. Variety Dough Quality Data Distribution over Analysis Years and Varieties.

| | ERS[a] (%) | | | | MSE (%) | | | | MPT (minutes) | | | | MPV (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Beadle | 4 | 13.74 | 0.71 | 1.30 | 4 | 20.52 | 0.68 | -2.22 | 4 | 1.89 | -1.64 | 3.08 | 4 | 12.82 | -0.58 | 0.86 |
| Brookings | 71 | 14.18 | -0.72 | 0.48 | 71 | 69.10 | 1.24 | 1.50 | 71 | 6.80 | 0.90 | 1.75 | 71 | 18.15 | -0.07 | -0.66 |
| Brown | 157 | 24.04 | -1.36 | 2.94 | 157 | 65.86 | 0.82 | 0.87 | 157 | 5.37 | 0.28 | -0.42 | 157 | 20.82 | 0.07 | 0.17 |
| Campbell | 18 | 6.35 | 0.83 | 0.24 | 18 | 43.60 | -0.05 | 0.04 | 18 | 4.25 | 0.33 | -0.09 | 18 | 10.24 | 0.52 | -0.55 |
| Charles Mix | 12 | 10.00 | -0.10 | -1.59 | 12 | 62.71 | 0.54 | -1.50 | 12 | 2.67 | -0.27 | -1.47 | 12 | 12.85 | -0.13 | -1.54 |
| Clark | 41 | 11.97 | -0.69 | 0.31 | 41 | 65.10 | 1.32 | 2.48 | 41 | 6.36 | 0.99 | 0.13 | 41 | 24.35 | -1.08 | 3.87 |
| Codington | 24 | 16.37 | -1.13 | 1.96 | 24 | 31.22 | 0.06 | -1.15 | 24 | 5.69 | 0.06 | -0.27 | 24 | 16.99 | 0.14 | -1.15 |
| Corson | 30 | 9.61 | -0.40 | -0.74 | 30 | 58.33 | 1.02 | 0.94 | 30 | 5.13 | 0.62 | -0.18 | 30 | 18.12 | -0.54 | 0.65 |
| Day | 226 | 24.70 | -1.36 | 3.81 | 226 | 63.95 | 0.94 | 0.82 | 226 | 5.60 | 0.42 | -0.09 | 226 | 23.50 | 0.21 | -0.10 |
| Deuel | 16 | 8.78 | -0.25 | -1.55 | 16 | 33.84 | 0.21 | -0.80 | 16 | 3.16 | -0.55 | -0.55 | 16 | 10.69 | -0.29 | -0.30 |
| Dewey | 11 | 5.14 | 1.19 | 1.67 | 11 | 53.79 | 1.24 | 2.09 | 11 | 3.59 | 0.42 | -0.71 | 11 | 15.42 | 0.50 | 0.67 |
| Douglas | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Edmunds | 45 | 15.29 | -1.02 | 2.79 | 45 | 43.67 | 0.88 | 0.06 | 45 | 4.25 | 0.25 | -0.96 | 45 | 15.33 | 0.64 | -0.02 |
| Faulk | 57 | 15.51 | -1.65 | 4.11 | 57 | 78.68 | 1.26 | 1.92 | 57 | 6.66 | 0.68 | 0.79 | 57 | 21.71 | 0.06 | 0.74 |
| Grant | 14 | 10.29 | -0.11 | -0.57 | 14 | 37.64 | 0.94 | -0.26 | 14 | 2.18 | 0.74 | -0.45 | 14 | 10.21 | -0.33 | 0.07 |
| Hamlin | 7 | 4.51 | 1.15 | 1.26 | 7 | 22.75 | 0.95 | -0.24 | 7 | 2.30 | 0.46 | -0.87 | 7 | 5.31 | -0.15 | -0.96 |
| Hand | 85 | 14.34 | -0.63 | 0.23 | 85 | 59.30 | 1.06 | 1.43 | 85 | 4.35 | 0.27 | -0.16 | 85 | 17.44 | -0.12 | -0.66 |
| Hanson | 2 | 1.66 | - | - | 2 | 18.17 | - | - | 2 | 0.72 | - | - | 2 | 3.78 | - | - |
| Hughes | 7 | 11.51 | -1.62 | 2.71 | 7 | 17.73 | -0.96 | -0.38 | 7 | 3.64 | -0.39 | 0.30 | 7 | 14.59 | 1.11 | 2.39 |
| Hutchinson | 3 | 5.79 | -0.99 | - | 3 | 12.32 | 0.72 | - | 3 | 1.75 | 1.05 | - | 3 | 9.69 | -0.70 | - |
| Hyde | 7 | 6.87 | 0.20 | -1.27 | 7 | 10.20 | 2.25 | 5.43 | 7 | 2.44 | -0.70 | -0.01 | 7 | 5.78 | 0.11 | -2.51 |
| Jerauld | 17 | 11.33 | -0.10 | -0.37 | 17 | 43.90 | 0.85 | -0.57 | 17 | 3.26 | -0.04 | -0.38 | 17 | 11.24 | 1.00 | 1.39 |
| Jones | 23 | 11.61 | -0.52 | -0.45 | 23 | 60.75 | 1.44 | 2.48 | 23 | 4.76 | 0.18 | -0.95 | 23 | 16.20 | 1.08 | 2.76 |
| Kingsbury | 7 | 5.57 | -0.07 | -1.56 | 7 | 53.28 | 0.32 | -0.57 | 7 | 2.77 | -0.41 | -2.11 | 7 | 6.76 | 0.25 | -0.47 |
| Lake | 18 | 12.40 | -1.01 | 0.54 | 18 | 57.77 | 0.61 | -1.00 | 18 | 3.98 | 1.49 | 3.08 | 18 | 12.75 | 0.18 | -0.72 |
| Lyman | 8 | 5.44 | -0.53 | -0.90 | 8 | 18.22 | 1.14 | 1.30 | 8 | 3.06 | -0.01 | -1.16 | 8 | 14.21 | -0.85 | -1.00 |
| Marshall | 16 | 9.52 | -0.33 | -0.67 | 16 | 52.08 | 1.61 | 1.84 | 16 | 2.96 | 0.38 | -1.20 | 16 | 14.90 | 0.00 | -0.79 |
| McPherson | 50 | 10.64 | -0.70 | 0.55 | 50 | 71.83 | 1.39 | 1.85 | 50 | 3.92 | 0.14 | -0.16 | 50 | 19.65 | 1.28 | 2.28 |
| Minnehaha | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Moody | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Pennington | 6 | 22.29 | -1.20 | 0.40 | 6 | 38.74 | -0.11 | -2.74 | 6 | 2.57 | -0.63 | 0.41 | 6 | 15.01 | -0.65 | -1.85 |
| Potter | 80 | 11.78 | -0.36 | -0.47 | 80 | 71.97 | 1.50 | 3.39 | 80 | 5.31 | 0.57 | -0.07 | 80 | 16.48 | 0.01 | -0.33 |
| Roberts | 28 | 11.54 | -0.39 | -0.73 | 28 | 64.01 | 1.73 | 4.31 | 28 | 4.71 | 0.51 | -0.83 | 28 | 12.60 | 0.28 | 0.24 |
| Sanborn | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Spink | 76 | 20.59 | -1.59 | 3.93 | 76 | 58.83 | 1.12 | 1.12 | 76 | 5.52 | 0.65 | 0.05 | 76 | 21.66 | -0.09 | 0.04 |
| Sully | 31 | 12.18 | -0.60 | -0.50 | 31 | 39.64 | 0.98 | 0.36 | 31 | 4.09 | -0.12 | -1.08 | 31 | 16.46 | 0.69 | 0.58 |
| Tripp | 24 | 8.58 | -0.51 | -0.72 | 24 | 44.44 | 0.37 | 0.49 | 24 | 4.36 | -0.29 | -0.46 | 24 | 16.21 | -0.59 | -0.22 |
| Walworth | 198 | 14.11 | -0.61 | 0.03 | 198 | 72.39 | 1.78 | 4.02 | 198 | 5.91 | 0.39 | -0.47 | 198 | 23.07 | 0.15 | 0.00 |

[a]ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value.

[b]N: Sample Size.

Table 2.37. District Dough Quality Data Distribution over Analysis Years and Varieties.

| | ERS[a] (%) | | | | MSE (%) | | | | MPT (minutes) | | | | MPV (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Central | 144 | 15.84 | -0.49 | -0.10 | 144 | 59.30 | 1.09 | 1.10 | 144 | 4.39 | 0.09 | -0.61 | 144 | 20.84 | 0.18 | -0.26 |
| East Central | 107 | 14.18 | -0.93 | 0.82 | 107 | 69.10 | 1.08 | 0.76 | 107 | 6.80 | 0.84 | 1.21 | 107 | 20.02 | 0.08 | -0.29 |
| North Central | 681 | 24.04 | -1.21 | 2.98 | 681 | 81.33 | 1.30 | 2.23 | 681 | 6.66 | 0.49 | -0.08 | 681 | 28.78 | 0.17 | 0.44 |
| North East | 372 | 24.70 | -1.12 | 2.71 | 372 | 73.52 | 1.10 | 1.61 | 372 | 6.70 | 0.65 | 0.32 | 372 | 29.97 | 0.05 | 0.34 |
| North West | 41 | 9.79 | -0.52 | -0.13 | 41 | 62.00 | 1.08 | 1.11 | 41 | 5.13 | 0.55 | -0.30 | 41 | 21.57 | -0.29 | 0.74 |
| South Central | 56 | 11.61 | -0.70 | -0.10 | 56 | 62.83 | 1.25 | 2.94 | 56 | 5.15 | 0.04 | -0.73 | 56 | 19.40 | -0.15 | -0.23 |
| South East | 16 | 10.00 | -0.10 | -1.28 | 16 | 62.71 | 0.91 | -0.64 | 16 | 2.81 | -0.24 | -0.97 | 16 | 16.17 | 0.07 | -1.16 |
| West Central | 6 | 22.29 | -1.20 | 0.40 | 6 | 38.74 | -0.11 | -2.74 | 6 | 2.57 | -0.63 | 0.41 | 6 | 15.01 | -0.65 | -1.85 |

[a]ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value.

[b]N: Sample Size.

Table 2.38. Year Dough Quality Data Distribution over Analysis Varieties and Production Environments.

| | ERS[a] (%) | | | | MSE (%) | | | | MPT (minutes) | | | | MPV (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| 2008 | 19 | 21.35 | -2.10 | 6.07 | 19 | 68.21 | 1.61 | 3.81 | 19 | 4.36 | 0.73 | 1.23 | 19 | 29.97 | -0.40 | 2.81 |
| 2009 | 348 | 21.09 | -1.08 | 2.09 | 348 | 81.33 | 1.22 | 1.31 | 348 | 5.97 | 1.15 | 2.53 | 348 | 23.38 | -0.01 | -0.23 |
| 2010 | 252 | 17.13 | -0.81 | 0.58 | 252 | 70.35 | 1.12 | 1.07 | 252 | 4.50 | 0.63 | -0.26 | 252 | 23.65 | -0.31 | 0.62 |
| 2011 | 163 | 19.68 | -0.99 | 1.79 | 163 | 64.21 | 1.15 | 1.32 | 163 | 5.53 | 0.39 | -0.07 | 163 | 15.97 | 0.06 | -0.34 |
| 2012 | 402 | 24.04 | -1.41 | 4.67 | 402 | 68.29 | 1.04 | 1.31 | 402 | 6.25 | 0.69 | 0.35 | 402 | 26.39 | 0.43 | 1.07 |
| 2013 | 199 | 13.16 | -0.79 | 0.20 | 199 | 51.52 | 1.15 | 1.12 | 199 | 5.37 | 0.22 | 0.41 | 199 | 19.45 | -0.06 | -0.07 |
| 2015 | 40 | 13.13 | -0.14 | -0.45 | 40 | 40.35 | 1.20 | 1.48 | 40 | 3.01 | 0.49 | 0.40 | 40 | 16.53 | 0.04 | -0.51 |

[a]ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value.

[b]N: Sample Size.

Table 2.39. Variety Dough Quality Data Distribution over Analysis Years and Production Environments.

| | MLS[a] (%) | | | | MRS (%) | | | | MSM (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variety | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| ADVANCE | 68 | 10.73 | -0.02 | -0.47 | 68 | 5.65 | -0.62 | 1.28 | 68 | 13.59 | 0.39 | 0.61 |
| BARLOW | 89 | 9.49 | -0.31 | -0.30 | 89 | 4.66 | -0.06 | -0.17 | 89 | 11.13 | -0.11 | 0.00 |
| BRICK | 209 | 24.13 | 1.23 | 5.72 | 209 | 8.37 | -1.33 | 4.40 | 209 | 30.52 | 2.07 | 12.51 |
| BRIGGS | 287 | 22.51 | 0.63 | 1.69 | 287 | 9.18 | -0.31 | 0.73 | 287 | 26.43 | 0.92 | 2.77 |
| FALLER | 106 | 15.05 | 0.08 | 1.35 | 106 | 6.13 | -0.63 | 1.42 | 106 | 17.66 | 0.99 | 3.24 |
| FOREFRONT | 44 | 16.43 | 0.76 | 2.81 | 44 | 3.90 | 0.18 | -0.66 | 44 | 18.10 | 0.79 | 2.96 |
| HOWARD | 43 | 13.77 | 0.24 | 0.49 | 43 | 4.96 | 0.16 | -0.58 | 43 | 15.87 | 0.38 | 0.43 |
| PROSPER | 38 | 13.89 | 0.63 | 0.46 | 38 | 7.95 | -0.79 | 2.33 | 38 | 18.62 | 1.41 | 2.48 |
| RB07 | 208 | 16.44 | 0.01 | -0.15 | 208 | 8.91 | -0.54 | 0.92 | 208 | 20.71 | 0.56 | 1.12 |
| SELECT | 162 | 24.26 | 1.84 | 9.79 | 162 | 8.14 | -1.19 | 2.81 | 162 | 28.51 | 2.71 | 15.26 |
| STEELE-ND | 40 | 9.62 | -0.12 | -0.71 | 40 | 5.69 | -0.11 | 1.04 | 40 | 12.09 | -0.13 | -0.37 |
| TRAVERSE | 129 | 22.20 | 0.38 | 0.16 | 129 | 10.15 | -0.07 | 0.53 | 129 | 27.91 | 0.57 | 0.52 |

[a]MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

[b]N: Sample Size.

Table 2.40. Variety Dough Quality Data Distribution over Analysis Years and Varieties.

| | MLS [a](%) | | | | MRS (%) | | | | MSM (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| County | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Beadle | 4 | 10.88 | -1.24 | 1.51 | 4 | 5.20 | -1.65 | 2.74 | 4 | 14.14 | 0.11 | 0.13 |
| Brookings | 71 | 24.00 | 1.84 | 5.49 | 71 | 8.37 | -1.14 | 1.60 | 71 | 30.02 | 2.06 | 5.91 |
| Brown | 157 | 21.61 | 1.05 | 3.70 | 157 | 10.43 | -1.12 | 2.26 | 157 | 28.03 | 1.78 | 5.69 |
| Campbell | 18 | 8.82 | 0.45 | -0.66 | 18 | 5.08 | 0.20 | -0.32 | 18 | 9.36 | 0.39 | -1.12 |
| Charles Mix | 12 | 14.22 | 0.61 | -0.42 | 12 | 4.61 | 0.37 | -0.01 | 12 | 16.72 | 0.76 | -0.35 |
| Clark | 41 | 12.91 | 0.20 | 0.77 | 41 | 7.01 | -0.78 | 0.73 | 41 | 18.08 | 0.84 | 1.95 |
| Codington | 24 | 12.98 | 0.09 | -1.07 | 24 | 5.86 | -1.12 | 1.48 | 24 | 15.70 | 0.59 | -0.56 |
| Corson | 30 | 11.14 | 0.65 | 0.35 | 30 | 4.48 | 0.35 | -0.52 | 30 | 14.12 | 0.60 | 0.65 |
| Day | 226 | 14.00 | -0.11 | -0.54 | 226 | 6.50 | -0.78 | 0.32 | 226 | 16.90 | 0.40 | -0.19 |
| Deuel | 16 | 10.15 | 0.65 | -0.13 | 16 | 7.31 | -0.54 | -0.53 | 16 | 14.82 | 1.73 | 2.36 |
| Dewey | 11 | 10.62 | -0.88 | -0.03 | 11 | 3.23 | -0.15 | -0.33 | 11 | 10.71 | -0.12 | -0.31 |
| Douglas | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Edmunds | 45 | 13.06 | 0.41 | 0.57 | 45 | 4.89 | -0.59 | -0.11 | 45 | 14.56 | 0.78 | 1.91 |
| Faulk | 57 | 19.44 | 0.52 | 0.08 | 57 | 10.14 | -1.11 | 3.33 | 57 | 27.11 | 1.06 | 1.49 |
| Grant | 14 | 6.74 | -0.71 | 0.12 | 14 | 3.84 | -0.79 | -0.45 | 14 | 8.25 | -0.95 | 0.32 |
| Hamlin | 7 | 5.61 | 0.59 | -0.23 | 7 | 1.66 | -0.38 | -1.68 | 7 | 5.22 | 0.52 | -1.03 |
| Hand | 85 | 16.11 | 0.52 | -0.04 | 85 | 7.27 | -0.64 | 0.51 | 85 | 19.11 | 0.82 | 0.76 |
| Hanson | 2 | 5.20 | - | - | 2 | 2.81 | - | - | 2 | 8.01 | - | - |
| Hughes | 7 | 11.81 | -0.13 | 1.84 | 7 | 8.04 | -1.92 | 4.68 | 7 | 18.12 | 1.37 | 3.23 |
| Hutchinson | 3 | 11.89 | -1.47 | - | 3 | 3.70 | -1.43 | - | 3 | 12.51 | -1.65 | - |
| Hyde | 7 | 8.33 | 0.56 | -0.76 | 7 | 2.73 | -0.55 | -0.98 | 7 | 10.03 | 1.17 | 1.86 |
| Jerauld | 17 | 7.16 | 0.09 | -1.49 | 17 | 4.28 | 0.17 | -0.25 | 17 | 9.66 | 0.25 | -0.96 |
| Jones | 23 | 12.35 | -0.09 | -0.40 | 23 | 6.49 | -0.67 | -0.72 | 23 | 18.29 | 0.26 | -0.20 |
| Kingsbury | 7 | 6.64 | -1.57 | 3.59 | 7 | 3.30 | -1.38 | 1.40 | 7 | 9.83 | -0.30 | 1.99 |
| Lake | 18 | 12.87 | 0.63 | 0.05 | 18 | 5.51 | -0.30 | -0.72 | 18 | 16.72 | 0.77 | 0.96 |
| Lyman | 8 | 9.08 | 0.16 | -1.00 | 8 | 6.08 | -0.53 | -1.09 | 8 | 12.08 | 0.18 | -1.68 |
| Marshall | 16 | 9.68 | 0.24 | 0.05 | 16 | 5.08 | 0.07 | -0.93 | 16 | 10.81 | 0.14 | -0.86 |
| McPherson | 50 | 15.43 | 0.71 | 0.83 | 50 | 8.05 | -0.40 | 0.26 | 50 | 17.68 | 0.62 | 0.53 |
| Minnehaha | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Moody | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Pennington | 6 | 8.01 | -0.56 | -1.83 | 6 | 2.80 | 0.26 | -1.35 | 6 | 9.71 | -0.52 | -1.39 |
| Potter | 80 | 14.13 | 0.35 | 0.03 | 80 | 5.75 | -0.30 | -0.99 | 80 | 17.86 | 0.56 | 0.37 |
| Roberts | 28 | 14.63 | 0.20 | 0.80 | 28 | 4.29 | 0.18 | -0.87 | 28 | 15.29 | 0.22 | 0.78 |
| Sanborn | 1 | 0.00 | - | - | 1 | 0.00 | - | - | 1 | 0.00 | - | - |
| Spink | 76 | 16.68 | 0.36 | 1.43 | 76 | 6.57 | -0.60 | 0.36 | 76 | 20.81 | 1.09 | 3.48 |
| Sully | 31 | 14.67 | 0.23 | 0.07 | 31 | 7.14 | -0.38 | -0.23 | 31 | 15.78 | 1.06 | 0.50 |
| Tripp | 24 | 22.31 | 2.13 | 6.37 | 24 | 5.35 | 0.04 | -0.44 | 24 | 25.52 | 2.39 | 7.32 |
| Walworth | 198 | 14.92 | 0.03 | -0.25 | 198 | 5.75 | -0.48 | -0.18 | 198 | 14.86 | 0.29 | -0.43 |

[a]MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

[b]N: Sample Size.

Table 2.41. District Dough Quality Data Distribution over Analysis Years and Varieties.

| | MLS[a] (%) | | | | MRS (%) | | | | MSM (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| District | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| Central | 144 | 16.43 | 0.41 | -0.09 | 144 | 7.32 | -0.66 | 0.53 | 144 | 19.81 | 0.84 | 0.63 |
| East Central | 107 | 24.00 | 1.61 | 5.10 | 107 | 9.28 | -1.12 | 1.59 | 107 | 30.02 | 1.81 | 5.07 |
| North Central | 681 | 21.96 | 0.64 | 1.59 | 681 | 11.35 | -0.84 | 1.55 | 681 | 28.87 | 1.22 | 3.58 |
| North East | 372 | 14.63 | 0.04 | -0.23 | 372 | 7.87 | -0.81 | 0.60 | 372 | 19.24 | 0.60 | 0.59 |
| North West | 41 | 12.11 | 0.21 | -0.56 | 41 | 4.48 | 0.22 | -0.58 | 41 | 14.12 | 0.39 | -0.02 |
| South Central | 56 | 22.31 | 1.39 | 4.50 | 56 | 6.49 | -0.33 | -0.79 | 56 | 27.06 | 1.32 | 3.46 |
| South East | 16 | 14.22 | 0.49 | -1.15 | 16 | 4.89 | -0.16 | -0.49 | 16 | 16.72 | 0.53 | -1.19 |
| West Central | 6 | 8.01 | -0.56 | -1.83 | 6 | 2.80 | 0.26 | -1.35 | 6 | 9.71 | -0.52 | -1.39 |

[a]MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

[b]N: Sample Size.

Table 2.42. Year Dough Quality Data Distribution over Analysis Varieties and Production Environments.

| | MLS[a] (%) | | | | MRS (%) | | | | MSM (%) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | N[b] | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis | N | Range | Skewness | Kurtosis |
| 2008 | 19 | 11.29 | 0.35 | 0.13 | 19 | 4.85 | 0.12 | 0.27 | 19 | 15.34 | 0.38 | 0.30 |
| 2009 | 348 | 24.33 | 0.79 | 2.63 | 348 | 10.15 | -0.70 | 1.04 | 348 | 29.27 | 1.26 | 3.77 |
| 2010 | 252 | 23.16 | 0.56 | 1.41 | 252 | 9.20 | -0.32 | 0.14 | 252 | 26.09 | 0.86 | 1.46 |
| 2011 | 163 | 17.08 | 0.72 | 1.31 | 163 | 6.87 | -0.69 | 0.26 | 163 | 19.05 | 1.14 | 2.79 |
| 2012 | 402 | 16.52 | 0.00 | -0.06 | 402 | 7.76 | -0.62 | 0.79 | 402 | 15.82 | 0.21 | 0.06 |
| 2013 | 199 | 11.82 | 0.12 | -0.31 | 199 | 4.79 | 0.04 | -0.39 | 199 | 14.22 | 0.33 | 0.13 |
| 2015 | 40 | 9.26 | -0.35 | -0.87 | 40 | 3.70 | 0.05 | -0.20 | 40 | 10.47 | -0.08 | -0.69 |

[a]MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

[b]N: Sample Size.

Table 2.43. Variety Shapiro-Wilk Test[a] for Normal Distribution for kernel quality traits over Analysis Years and Production Environments.

| Variety | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| ADVANCE | 0.97 | 0.98 | 0.96* |
| BARLOW | 0.98 | 0.98 | 0.96** |
| BRICK | 0.99* | 0.99 | 0.92** |
| BRIGGS | 0.99* | 0.96** | 0.95** |
| FALLER | 0.98 | 0.9** | 0.97** |
| FOREFRONT | 0.99 | 0.94* | 0.92** |
| HOWARD | 0.97 | 0.98 | 0.96 |
| PROSPER | 0.99 | 0.9** | 0.96 |
| RB07 | 0.99 | 0.95** | 0.94** |
| SELECT | 0.99 | 0.99 | 0.94** |
| STEELE-ND | 0.95 | 0.86** | 0.89** |
| TRAVERSE | 0.98 | 0.95** | 0.97** |

[a]*, ** Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

Table 2.44. Variety Shapiro-Wilk Test[a] for Normal Distribution for flour quality traits over Analysis Years and Production Environments.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| ADVANCE | 0.94** | 0.93** | 0.98 | 0.56** | 0.99 | 0.99 | 0.99 |
| BARLOW | 0.99 | 0.95** | 0.98 | 0.91** | 0.99 | 0.92** | 0.99 |
| BRICK | 0.99 | 0.97** | 0.99 | 0.61** | 0.98** | 0.94** | 0.99 |
| BRIGGS | 0.98** | 0.97** | 0.98** | 0.98** | 0.98** | 0.98** | 0.99** |
| FALLER | 0.98 | 0.98 | 0.99 | 0.84** | 0.99 | 0.99 | 0.99 |
| FOREFRONT | 0.97 | 0.93** | 0.98 | 0.85** | 0.99 | 0.98 | 0.99 |
| HOWARD | 0.93** | 0.98 | 0.97 | 0.86** | 0.98 | 0.97 | 0.98 |
| PROSPER | 0.94* | 0.97 | 0.97 | 0.73** | 0.97 | 0.98 | 0.96 |
| RB07 | 0.99 | 0.96** | 0.99* | 0.81** | 0.94** | 0.84** | 0.97** |
| SELECT | 0.99 | 0.97** | 0.98* | 0.82** | 0.98* | 0.99 | 0.99 |
| STEELE-ND | 0.97 | 0.93** | 0.97 | 0.81** | 0.96 | 0.97 | 0.96 |
| TRAVERSE | 0.99 | 0.97** | 0.99 | 0.98 | 0.98* | 0.98 | 0.98* |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

Table 2.45. Variety Shapiro-Wilk Test[a] for Normal Distribution for dough quality traits over Analysis Years and Production Environments.

| Variety | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ADVANCE | 0.98 | 0.99 | 0.98 | 0.88** | 0.97 | 0.93** | 0.99 | 0.99 | 0.99 | 0.97 | 0.98 |
| BARLOW | 0.98 | 0.99 | 0.99 | 0.9** | 0.95** | 0.92** | 0.99 | 0.99 | 0.98 | 1 | 0.99 |
| BRICK | 0.99 | 1 | 0.99 | 0.85** | 0.96** | 0.89** | 0.99 | 0.97** | 0.93** | 0.93** | 0.88** |
| BRIGGS | 0.98** | 0.92** | 0.99 | 0.86** | 0.96** | 0.88** | 0.91** | 0.99 | 0.98** | 0.99 | 0.96** |
| FALLER | 0.99 | 0.99 | 0.99 | 0.95** | 0.95** | 0.95** | 0.96** | 0.98 | 0.98 | 0.97* | 0.95** |
| FOREFRONT | 0.98 | 0.99 | 0.95 | 0.93** | 0.93** | 0.92** | 0.96 | 0.97 | 0.94* | 0.98 | 0.94* |
| HOWARD | 0.97 | 0.96 | 0.97 | 0.89** | 0.94* | 0.9** | 0.98 | 0.98 | 0.98 | 0.98 | 0.98 |
| PROSPER | 0.97 | 0.98 | 0.95 | 0.88** | 0.79** | 0.91** | 0.95 | 0.98 | 0.96 | 0.94 | 0.89** |
| RB07 | 0.99* | 0.99 | 0.98** | 0.88** | 0.93** | 0.9** | 0.97** | 1 | 0.99 | 0.98** | 0.98** |
| SELECT | 0.98* | 0.99 | 0.99 | 0.93** | 0.96** | 0.93** | 0.98* | 0.99 | 0.89** | 0.94** | 0.82** |
| STEELE-ND | 0.97 | 0.98 | 0.98 | 0.89** | 0.94* | 0.89** | 0.97 | 0.99 | 0.98 | 0.98 | 0.98 |
| TRAVERSE | 0.99 | 0.9** | 0.98 | 0.9** | 0.95** | 0.91** | 0.85** | 0.99 | 0.98 | 0.99 | 0.97** |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 2.46. Year Shapiro-Wilk Test[a] for kernel quality traits over Analysis Varieties and Production Environments.

| Variety | GPC[b] (12% moisture basis) | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| 2008 | 0.84** | 0.95 | 0.96 |
| 2009 | 0.99 | 0.99* | 0.98** |
| 2010 | 0.99* | 0.99* | 0.92** |
| 2011 | 0.96** | 0.99 | 0.96** |
| 2012 | 1.00 | 1.00 | 0.96** |
| 2013 | 1.00 | 0.99 | 0.97** |
| 2015 | 0.98 | 0.96 | 0.96 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.
[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

Table 2.47. Year Shapiro-Wilk Test[a] for flour quality traits over Analysis Varieties and Production Environments.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| 2008 | 0.87** | 0.9* | 0.86** | 0.85** | 0.83** | 0.86** | 0.85** |
| 2009 | 1 | 0.95** | 1 | 0.89** | 1 | 0.99* | 0.99 |
| 2010 | 0.99 | 0.96** | 0.98** | 0.88** | 0.98** | 0.92** | 0.99* |
| 2011 | 0.99 | 0.96** | 0.96** | 0.84** | 0.96** | 0.96** | 0.97** |
| 2012 | 0.99* | 0.99** | 0.99 | 0.75** | 1 | 0.97** | 1 |
| 2013 | 0.99* | 0.98* | 1 | 0.68** | 0.99 | 0.99 | 0.99 |
| 2015 | 0.95 | 0.99 | 0.97 | 0.77** | 0.98 | 0.96 | 0.98 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.
[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

Table 2.48. Year Shapiro-Wilk Test[a] for dough quality traits over Analysis Varieties and Production Environments.

| Variety | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2008 | 0.86** | 0.95 | 0.93 | 0.84** | 0.8** | 0.87* | 0.95 | 0.93 | 0.93 | 0.98 | 0.96 |
| 2009 | 1 | 0.95** | 0.99 | 0.89** | 0.94** | 0.9** | 0.94** | 1 | 0.96** | 0.97** | 0.93** |
| 2010 | 0.98** | 0.94** | 0.98** | 0.9** | 0.96** | 0.91** | 0.96** | 0.99 | 0.98** | 0.99* | 0.96** |
| 2011 | 0.96** | 0.97** | 0.99 | 0.89** | 0.95** | 0.92** | 0.98** | 0.99 | 0.97** | 0.96** | 0.93** |
| 2012 | 0.99 | 0.98** | 1 | 0.9** | 0.92** | 0.94** | 0.97** | 0.99** | 0.99** | 0.98** | 0.99 |
| 2013 | 1 | 0.99 | 0.99 | 0.9** | 0.95** | 0.91** | 0.99 | 0.99 | 0.99 | 0.99 | 0.99 |
| 2015 | 0.97 | 0.99 | 0.97 | 0.92** | 0.98 | 0.9** | 0.97 | 0.98 | 0.96 | 0.99 | 0.97 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 2.49. County Shapiro-Wilk Test[a] for Normal Distribution for kernel quality traits over Analysis Years and Varieties.

| Variety | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| Beadle | 0.97 | 0.91 | 0.9 |
| Brookings | 0.99 | 0.97 | 0.98 |
| Brown | 0.99 | 0.98 | 0.98** |
| Campbell | 0.86** | 0.83** | 0.92 |
| Charles Mix | 0.94 | 0.96 | 0.97 |
| Clark | 0.95 | 0.95 | 0.95 |
| Codington | 0.96 | 0.91* | 0.92* |
| Corson | 0.95 | 0.97 | 0.94 |
| Day | 0.97** | 1 | 0.94** |
| Deuel | 0.86* | 0.93 | 0.97 |
| Dewey | 0.95 | 0.93 | 0.91 |
| Douglas | - | - | - |
| Edmunds | 0.92** | 0.96 | 0.96 |
| Faulk | 0.96* | 0.96* | 0.9** |
| Grant | 0.9 | 0.98 | 0.86* |
| Hamlin | 0.79* | 0.82 | 0.83 |
| Hand | 0.97* | 0.98 | 0.94** |
| Hanson | 1 | 1 | 1 |
| Hughes | 0.72** | 0.82 | 0.96 |
| Hutchinson | 0.75** | 0.77* | 0.78 |
| Hyde | 0.79* | 0.83 | 0.89 |
| Jerauld | 0.91 | 0.87* | 0.91 |
| Jones | 0.95 | 0.87** | 0.91* |
| Kingsbury | 0.83 | 0.9 | 0.91 |
| Lake | 0.95 | 0.85** | 0.98 |
| Lyman | 0.82* | 0.91 | 0.86 |
| Marshall | 0.94 | 0.92 | 0.96 |
| McPherson | 0.95* | 0.94** | 0.96 |
| Minnehaha | - | - | - |
| Moody | - | - | - |
| Pennington | 0.97 | 0.89 | 0.96 |
| Potter | 0.98 | 0.98 | 0.93** |
| Roberts | 0.92* | 0.97 | 0.74** |
| Sanborn | - | - | - |
| Spink | 0.97 | 0.96* | 0.97 |
| Sully | 0.97 | 0.97 | 0.95 |
| Tripp | 0.94 | 0.96 | 0.98 |
| Walworth | 0.99 | 0.99 | 0.95** |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.
[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

Table 2.50. County Shapiro-Wilk Test[a] for Normal Distribution for flour quality traits over Analysis Years and Varieties.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| Beadle | 0.86 | 0.93 | 0.75* | 0.75* | 0.99 | 0.91 | 0.98 |
| Brookings | 0.98 | 0.94** | 0.96* | 0.82** | 0.98 | 0.98 | 0.98 |
| Brown | 0.98 | 0.93** | 0.99 | 0.83** | 0.98* | 0.95** | 0.98* |
| Campbell | 0.97 | 0.95 | 0.88* | 0.87* | 0.97 | 0.95 | 0.96 |
| Charles Mix | 0.96 | 0.99 | 0.95 | 0.87 | 0.97 | 0.96 | 0.95 |
| Clark | 0.96 | 0.93* | 0.95 | 0.78** | 0.94* | 0.92** | 0.94* |
| Codington | 0.96 | 0.96 | 0.95 | 0.7** | 0.97 | 0.97 | 0.97 |
| Corson | 0.97 | 0.89** | 0.95 | 0.9** | 0.93* | 0.78** | 0.96 |
| Day | 0.99 | 0.97** | 0.97** | 0.75** | 0.99* | 0.98** | 0.99 |
| Deuel | 0.9 | 0.92 | 0.91 | 0.73** | 0.88* | 0.95 | 0.86* |
| Dewey | 0.87 | 0.94 | 0.98 | 0.75** | 0.9 | 0.99 | 0.92 |
| Douglas | - | - | - | - | - | - | - |
| Edmunds | 0.95* | 0.96 | 0.94* | 0.92** | 0.97 | 0.98 | 0.97 |
| Faulk | 0.98 | 0.96* | 0.95* | 0.84** | 0.99 | 0.97 | 0.98 |
| Grant | 0.92 | 0.97 | 0.92 | 0.83** | 0.95 | 0.95 | 0.94 |
| Hamlin | 0.84 | 0.92 | 0.77* | 0.87 | 0.95 | 0.88 | 0.97 |
| Hand | 0.99 | 0.98 | 0.98 | 0.85** | 0.97 | 0.97* | 0.99 |
| Hanson | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| Hughes | 0.98 | 0.89 | 0.86 | 0.6** | 0.74** | 0.77* | 0.75** |
| Hutchinson | 0.99 | 1 | 0.83 | 0.77* | 0.82 | 0.79 | 0.84 |
| Hyde | 0.98 | 0.95 | 0.89 | 0.74** | 0.8* | 0.83 | 0.8* |
| Jerauld | 0.95 | 0.94 | 0.86* | 0.75** | 0.94 | 0.92 | 0.92 |
| Jones | 0.92 | 0.91* | 0.93 | 0.82** | 0.98 | 0.98 | 0.98 |
| Kingsbury | 0.84 | 0.81* | 0.85 | 0.75** | 0.92 | 0.96 | 0.86 |
| Lake | 0.92 | 0.91 | 0.96 | 0.93 | 0.92 | 0.85** | 0.95 |
| Lyman | 0.89 | 0.97 | 0.87 | 0.86 | 0.87 | 0.85 | 0.87 |
| Marshall | 0.97 | 0.9 | 0.94 | 0.92 | 0.95 | 0.93 | 0.93 |
| McPherson | 0.99 | 0.9** | 0.94* | 0.79** | 0.94** | 0.94* | 0.94* |
| Minnehaha | - | - | - | - | - | - | - |
| Moody | - | - | - | - | - | - | - |
| Pennington | 0.99 | 0.95 | 0.96 | 0.78* | 0.86 | 0.92 | 0.8 |
| Potter | 0.99 | 0.97* | 0.96** | 0.91** | 0.94** | 0.96** | 0.96* |
| Roberts | 0.98 | 0.88** | 0.95 | 0.84** | 0.94 | 0.93 | 0.94 |
| Sanborn | - | - | - | - | - | - | - |
| Spink | 0.99 | 0.97 | 0.98 | 0.79** | 0.98 | 0.99 | 0.98 |
| Sully | 0.96 | 0.94 | 0.98 | 0.74** | 0.86** | 0.89** | 0.89** |
| Tripp | 0.97 | 0.95 | 0.93 | 0.9* | 0.95 | 0.97 | 0.97 |
| Walworth | 0.99 | 0.97** | 0.99 | 0.72** | 0.99 | 0.95** | 0.99 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

Table 2.51. County Shapiro-Wilk Test[a] for Normal Distribution for dough quality traits over Analysis Years and Varieties.

| County | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Beadle | 0.75* | 0.8 | 0.83 | 0.96 | 0.97 | 0.87 | 0.83 | 0.98 | 0.92 | 0.84 | 1 |
| Brookings | 0.96* | 0.97* | 0.98 | 0.9** | 0.96* | 0.9** | 0.94** | 0.98 | 0.85** | 0.92** | 0.81** |
| Brown | 0.99 | 0.98* | 0.99 | 0.95** | 0.91** | 0.95** | 0.98* | 0.99 | 0.94** | 0.93** | 0.88** |
| Campbell | 0.88* | 0.93 | 0.92 | 0.98 | 0.91 | 0.98 | 0.97 | 0.94 | 0.93 | 0.95 | 0.92 |
| Charles Mix | 0.95 | 0.95 | 0.95 | 0.88 | 0.92 | 0.86 | 0.91 | 0.93 | 0.95 | 0.98 | 0.93 |
| Clark | 0.95 | 0.95 | 0.91** | 0.83** | 0.96 | 0.87** | 0.89** | 0.92** | 0.98 | 0.96 | 0.96 |
| Codington | 0.95 | 0.97 | 0.92* | 0.98 | 0.93 | 0.95 | 0.98 | 0.95 | 0.96 | 0.92 | 0.95 |
| Corson | 0.95 | 0.92* | 0.95 | 0.86** | 0.96 | 0.91* | 0.95 | 0.97 | 0.96 | 0.97 | 0.97 |
| Day | 0.97** | 0.98** | 0.99 | 0.9** | 0.92** | 0.94** | 0.98** | 0.99 | 0.99 | 0.95** | 0.98** |
| Deuel | 0.91 | 0.92 | 0.96 | 0.93 | 0.9 | 0.94 | 0.94 | 0.98 | 0.91 | 0.94 | 0.77** |
| Dewey | 0.98 | 0.94 | 0.89 | 0.89 | 0.9 | 0.9 | 0.95 | 0.97 | 0.91 | 0.97 | 0.96 |
| Douglas | - | - | - | - | - | - | - | - | - | - | - |
| Edmunds | 0.94* | 0.95 | 0.99 | 0.88** | 0.93** | 0.92** | 0.96 | 0.96 | 0.98 | 0.97 | 0.94* |
| Faulk | 0.95* | 0.96 | 0.96 | 0.92** | 0.88** | 0.91** | 0.97 | 0.98 | 0.96 | 0.93** | 0.93** |
| Grant | 0.92 | 0.87* | 0.92 | 0.89 | 0.97 | 0.88* | 0.91 | 0.97 | 0.95 | 0.9 | 0.91 |
| Hamlin | 0.77* | 0.84 | 0.91 | 0.87 | 0.92 | 0.88 | 0.96 | 0.94 | 0.95 | 0.92 | 0.94 |
| Hand | 0.98 | 0.98 | 0.98 | 0.91** | 0.97* | 0.93** | 0.99 | 0.99 | 0.97 | 0.97* | 0.96** |
| Hanson | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| Hughes | 0.86 | 0.91 | 0.87 | 0.98 | 0.82 | 0.88 | 0.98 | 0.92 | 0.94 | 0.78* | 0.87 |
| Hutchinson | 0.84 | 0.96 | 0.84 | 0.99 | 0.96 | 0.98 | 0.95 | 0.98 | 0.89 | 0.9 | 0.83 |
| Hyde | 0.89 | 0.92 | 0.98 | 0.9 | 0.93 | 0.7** | 0.96 | 0.82 | 0.94 | 0.94 | 0.91 |
| Jerauld | 0.86* | 0.96 | 0.92 | 0.84** | 0.97 | 0.88* | 0.98 | 0.94 | 0.89* | 0.95 | 0.95 |
| Jones | 0.93 | 0.95 | 0.93 | 0.86** | 0.95 | 0.86** | 0.95 | 0.92 | 0.98 | 0.91* | 0.98 |
| Kingsbury | 0.85 | 0.84 | 0.97 | 0.95 | 0.93 | 0.96 | 0.86 | 0.99 | 0.84 | 0.84 | 0.92 |
| Lake | 0.96 | 0.92 | 0.93 | 0.9 | 0.91 | 0.88* | 0.89* | 0.95 | 0.97 | 0.94 | 0.96 |
| Lyman | 0.87 | 0.9 | 0.91 | 0.9 | 0.93 | 0.92 | 0.94 | 0.83 | 0.96 | 0.91 | 0.91 |
| Marshall | 0.94 | 0.91 | 0.96 | 0.75** | 0.96 | 0.77** | 0.93 | 0.97 | 0.99 | 0.97 | 0.96 |
| McPherson | 0.94* | 0.98 | 0.97 | 0.86** | 0.96 | 0.87** | 0.98 | 0.91** | 0.97 | 0.99 | 0.97 |
| Minnehaha | - | - | - | - | - | - | - | - | - | - | - |
| Moody | - | - | - | - | - | - | - | - | - | - | - |
| Pennington | 0.96 | 0.93 | 0.93 | 0.94 | 0.86 | 0.85 | 0.97 | 0.83 | 0.88 | 0.9 | 0.91 |
| Potter | 0.96** | 0.95** | 0.98 | 0.86** | 0.97 | 0.88** | 0.97* | 0.98 | 0.98 | 0.96** | 0.97 |
| Roberts | 0.95 | 0.93* | 0.94 | 0.82** | 0.96 | 0.86** | 0.93 | 0.97 | 0.96 | 0.96 | 0.97 |
| Sanborn | - | - | - | - | - | - | - | - | - | - | - |
| Spink | 0.98 | 0.97 | 0.99 | 0.91** | 0.88** | 0.92** | 0.96* | 0.99 | 0.97 | 0.96** | 0.94** |
| Sully | 0.98 | 0.95 | 0.98 | 0.9** | 0.94 | 0.9** | 0.96 | 0.96 | 0.97 | 0.98 | 0.9** |
| Tripp | 0.93 | 0.94 | 0.95 | 0.94 | 0.95 | 0.97 | 0.98 | 0.96 | 0.8** | 0.98 | 0.76** |
| Walworth | 0.99 | 0.98** | 1 | 0.84** | 0.97** | 0.85** | 0.98** | 1 | 1 | 0.98** | 0.99* |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 2.52. District Shapiro-Wilk Test[a] for Normal Distribution for kernel quality traits over Analysis Years and Varieties.

| Variety | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| Central | 0.98 | 0.99 | 0.95** |
| East Central | 0.99 | 0.95** | 0.97** |
| North Central | 1 | 0.99** | 0.97** |
| North East | 0.99** | 0.99 | 0.94** |
| North West | 0.96 | 0.98 | 0.94* |
| South Central | 0.96 | 0.97 | 0.96 |
| South East | 0.93 | 0.97 | 0.9 |
| West Central | 0.97 | 0.89 | 0.96 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.
[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

Table 2.53. District Shapiro-Wilk Test[a] for Normal Distribution for flour quality traits over Analysis Years and Varieties.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| Central | 0.99 | 0.98* | 0.98* | 0.8** | 0.99 | 0.99 | 1 |
| East Central | 0.99 | 0.96** | 0.98 | 0.8** | 0.98 | 0.97** | 0.99 |
| North Central | 1 | 0.97** | 0.99* | 0.83** | 1* | 0.98** | 1 |
| North East | 0.99** | 0.96** | 0.99** | 0.75** | 0.99 | 0.99** | 1 |
| North West | 0.97 | 0.93* | 0.96 | 0.88** | 0.94* | 0.78** | 0.98 |
| South Central | 0.98 | 0.96* | 0.96 | 0.86** | 0.97 | 0.98 | 0.97 |
| South East | 0.95 | 0.98 | 0.95 | 0.86* | 0.97 | 0.95 | 0.95 |
| West Central | 0.99 | 0.95 | 0.96 | 0.78* | 0.86 | 0.92 | 0.8 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.
[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

Table 2.54. District Shapiro-Wilk Test[a] for Normal Distribution for dough quality traits over Analysis Years and Varieties.

| Variety | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Central | 0.98* | 0.98 | 0.99 | 0.9** | 0.98* | 0.92** | 0.99 | 0.99 | 0.98 | 0.97** | 0.95** |
| East Central | 0.98 | 0.97* | 0.99 | 0.9** | 0.94** | 0.91** | 0.96** | 0.99 | 0.89** | 0.93** | 0.86** |
| North Central | 0.99* | 0.98** | 1 | 0.9** | 0.94** | 0.91** | 0.98** | 1 | 0.97** | 0.96** | 0.94** |
| North East | 0.99** | 0.98** | 0.99** | 0.91** | 0.94** | 0.93** | 0.97** | 0.99 | 0.99 | 0.96** | 0.98** |
| North West | 0.96 | 0.93* | 0.98 | 0.88** | 0.97 | 0.92** | 0.96 | 0.98 | 0.98 | 0.98 | 0.99 |
| South Central | 0.96 | 0.96* | 0.96 | 0.91** | 0.94** | 0.91** | 0.98 | 0.99 | 0.91** | 0.96 | 0.92** |
| South East | 0.95 | 0.96 | 0.94 | 0.87* | 0.95 | 0.85** | 0.95 | 0.95 | 0.91 | 0.97 | 0.91 |
| West Central | 0.96 | 0.93 | 0.93 | 0.94 | 0.86 | 0.85 | 0.97 | 0.83 | 0.88 | 0.9 | 0.91 |

[a]*, **Correlations significant at $P < 0.05$ and $P < 0.01$, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

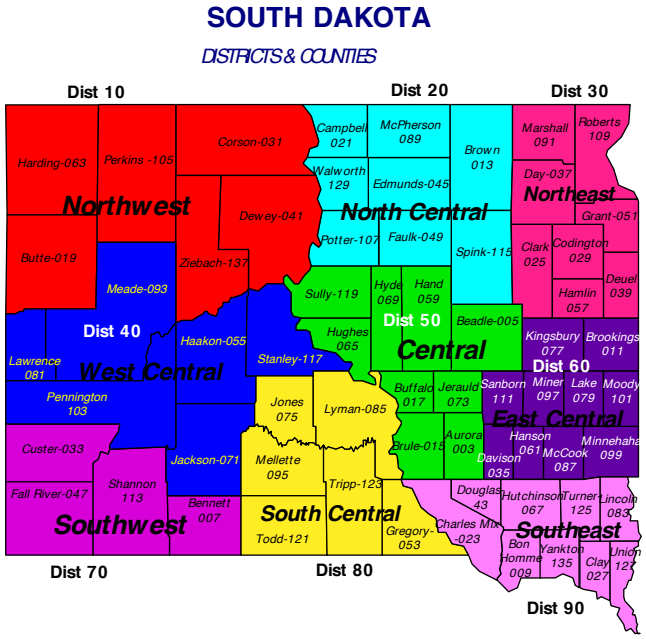
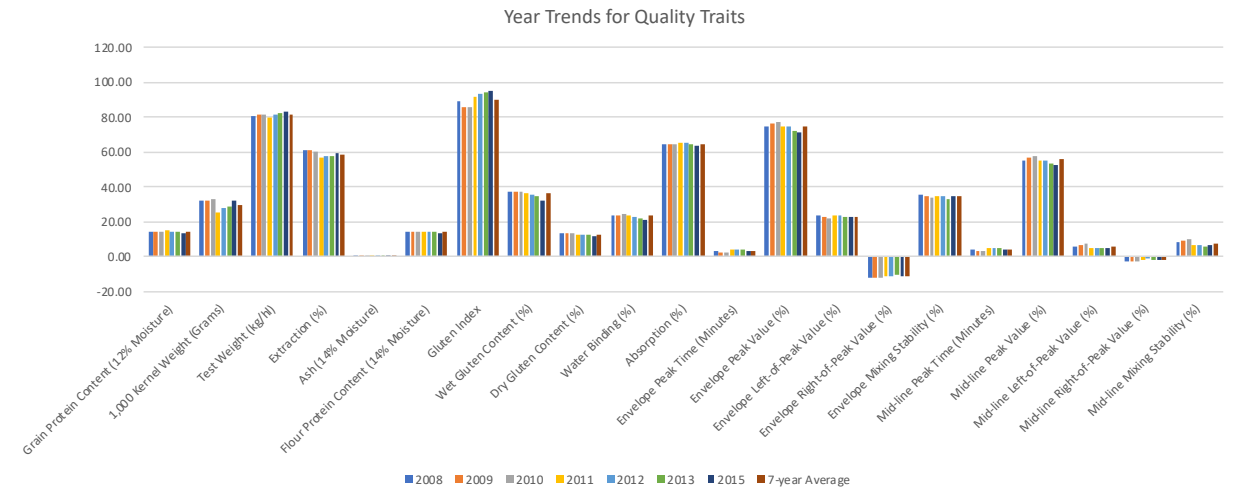



Figure 2.1. USDA, South Dakota Crop Reporting Districts



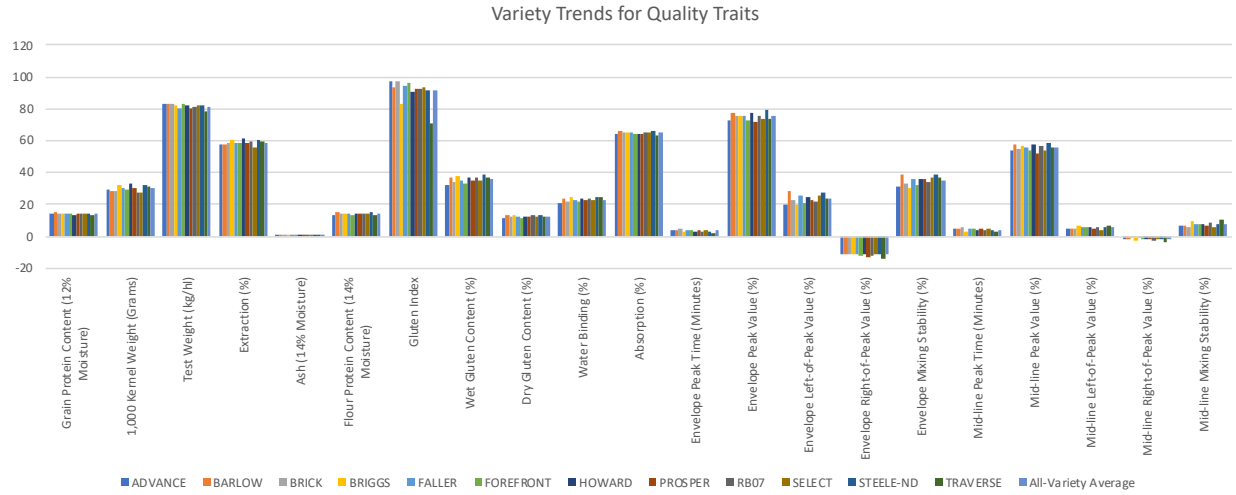




*Figure 2.2. Year and Variety Barplots for Quality Traits over Production Environments.*

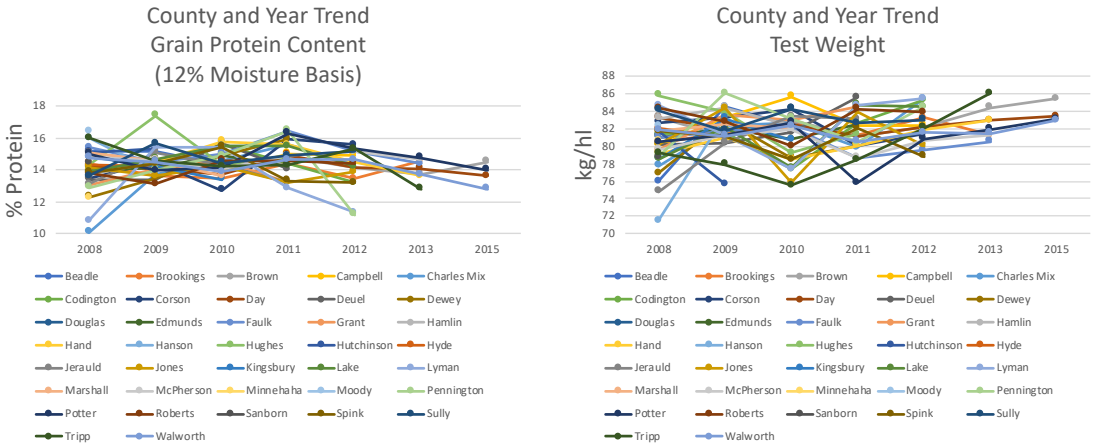



*Figure 2.3. County and Year line graph for grain protein content and test weight, respectively, over analysis varieties.*

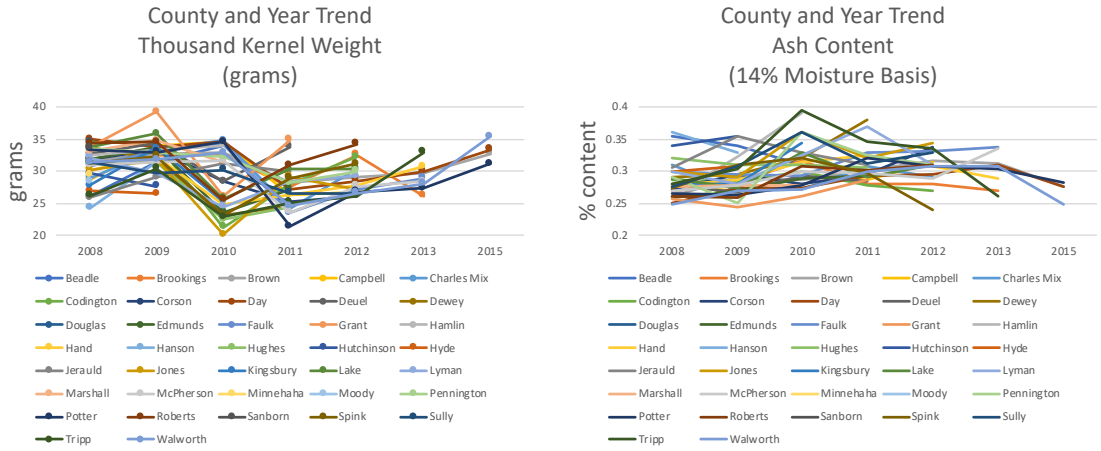



*Figure 2.4. County and year line graphs for thousand kernel weight and ash content, respectively, over analysis varieties.*

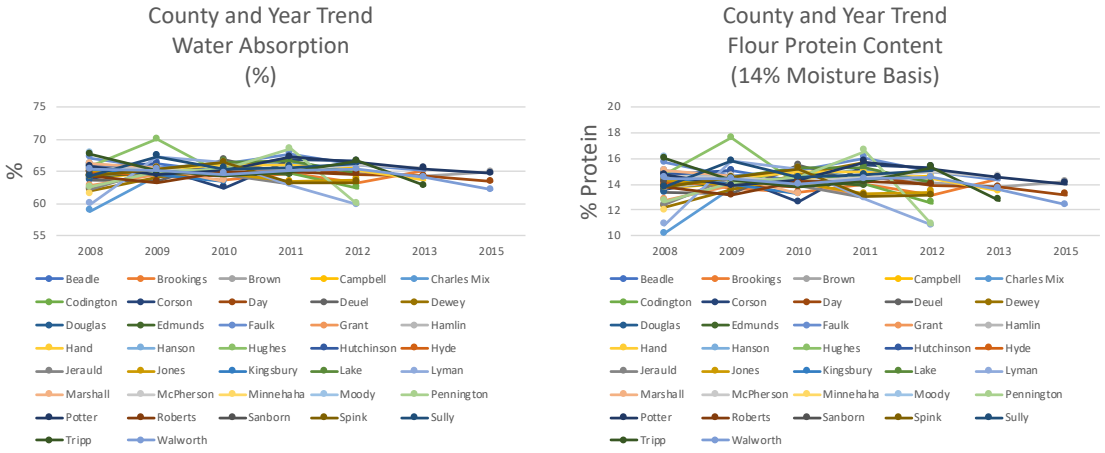



*Figure 2.5. County and Year line graphs for water absorption and flour protein content, over analysis varieties.*

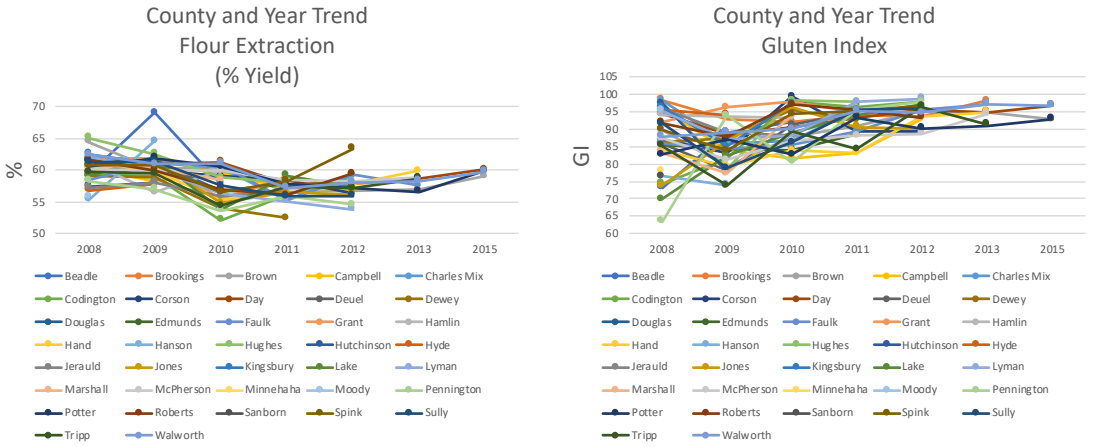



*Figure 2.6. County and Year line graphs for flour extraction and gluten index, respectively, over analysis varieties.*

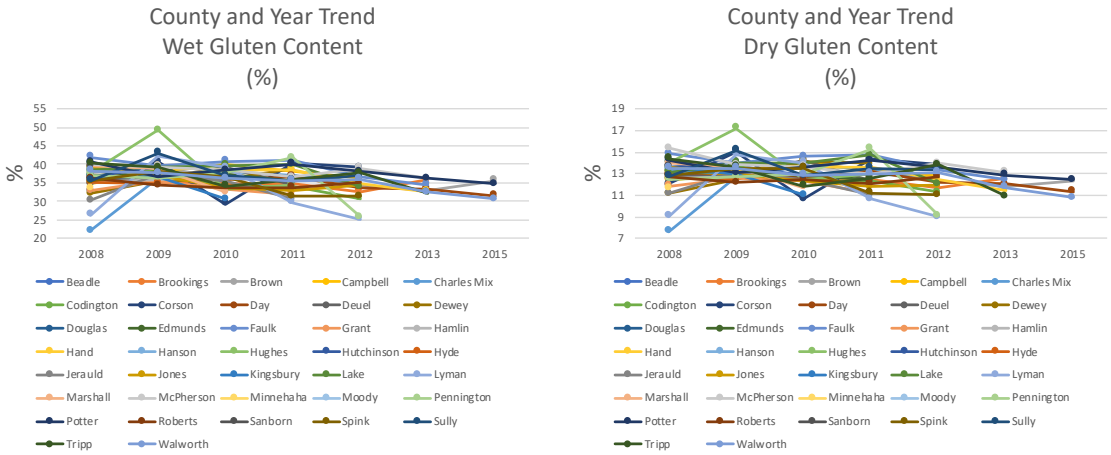



*Figure 2.7. County and Year line graphs for wet gluten content and dry gluten content, respectively, over analysis varieties.*

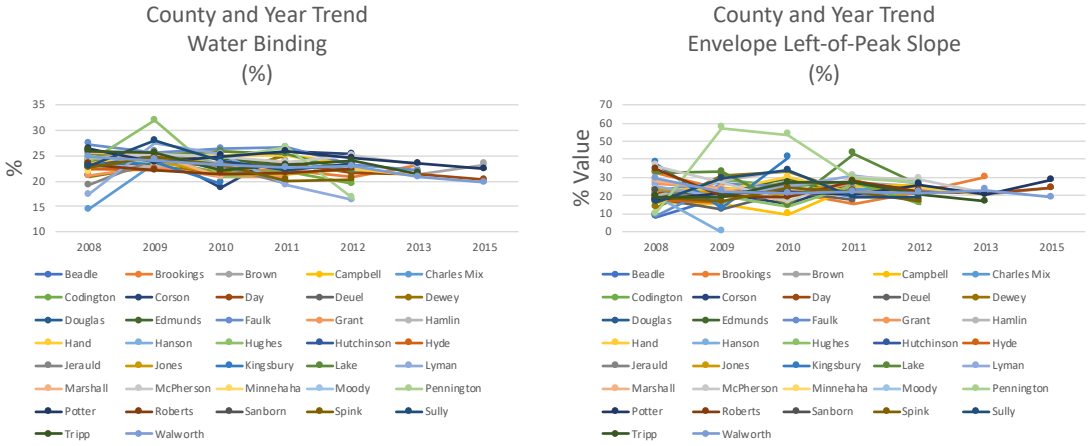



*Figure 2.8. County and Year line graphs for water binding and envelope left-of-peak slope, respectively, over analysis varieties.*

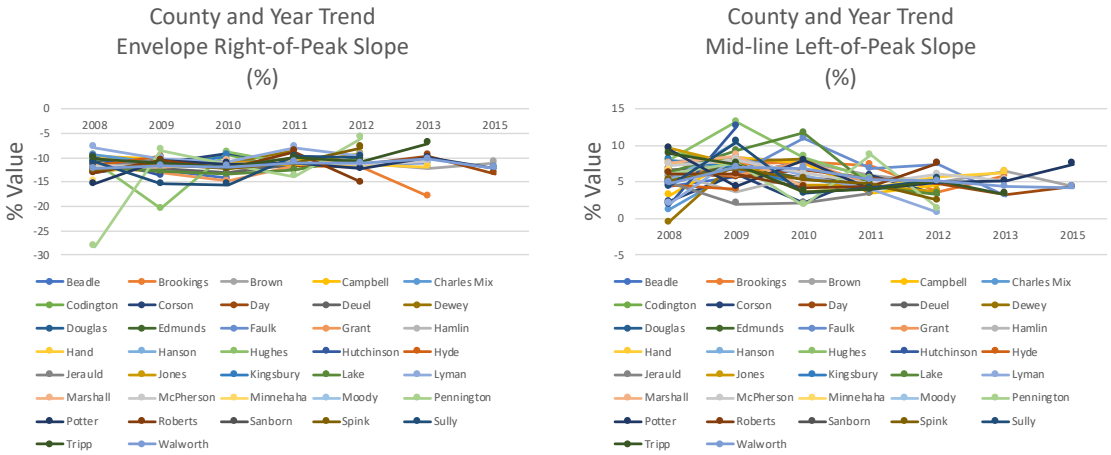



*Figure 2.9. County and Year line graphs for envelope peak time and envelope peak value, respectively, over analysis varieties.*

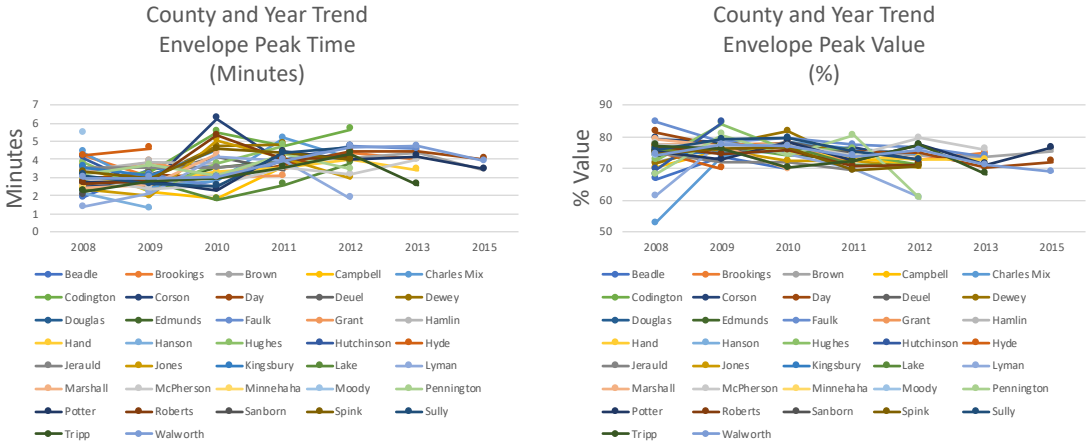



*Figure 2.10. County and Year line graphs for envelope right-of-peak slope and mid-line left-of-peak slope, respectively, over analysis varieties.*

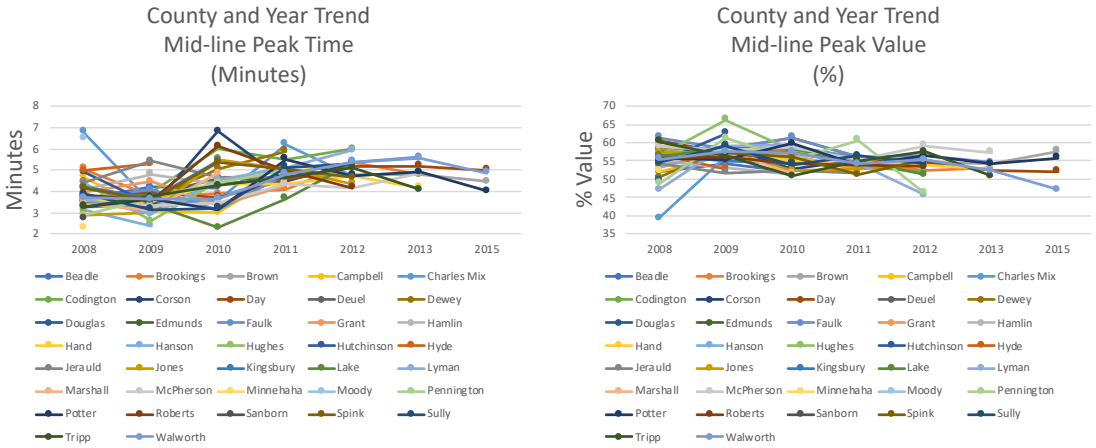



*Figure 2.11. County and Year line graphs for mid-line peak time and mid-line peak value, respectively, over analysis varieties.*

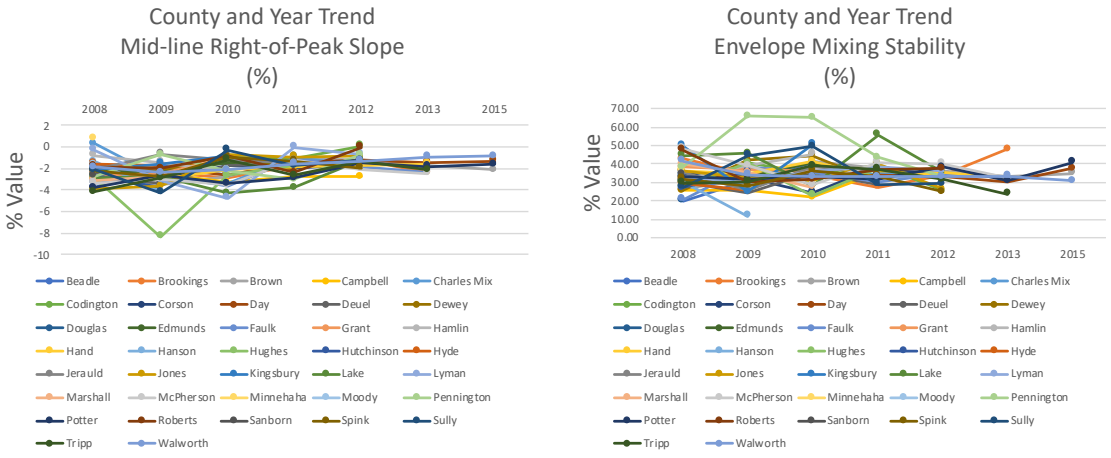



*Figure 2.12. County and Year line graphs for mid-line right-of-peak slope and envelope mixing stability, respectively, over analysis varieties.*

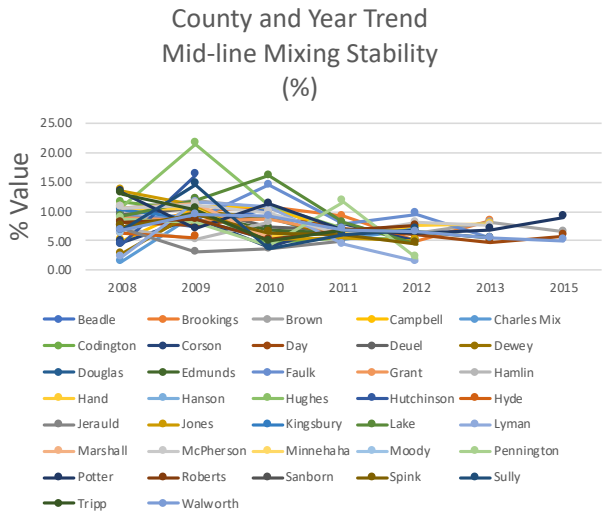



*Figure 2.13. County and Year line graphs for mid-line mixing stability, over analysis varieties.*

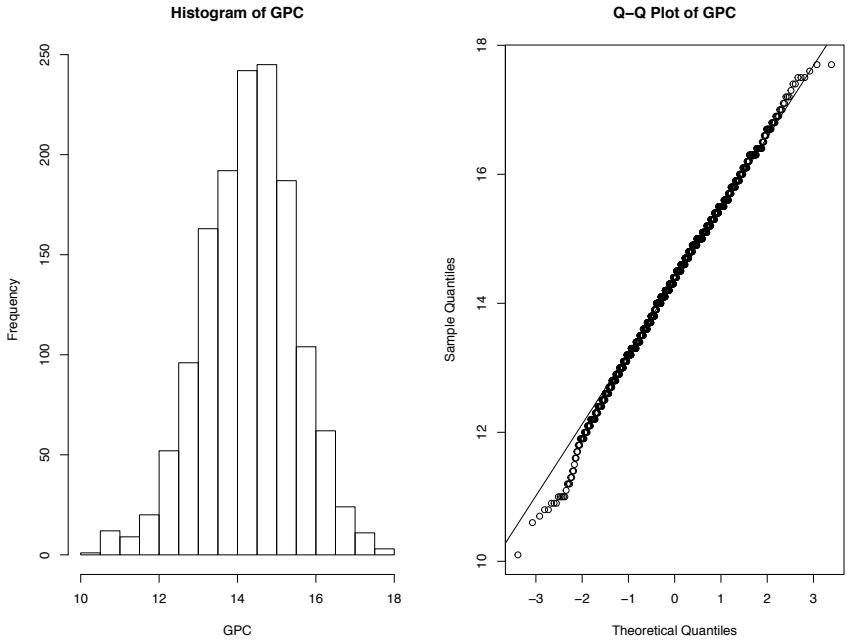



*Figure 2.14. Histogram and Q-Q Plot of Grain Protein Content (GPC).*

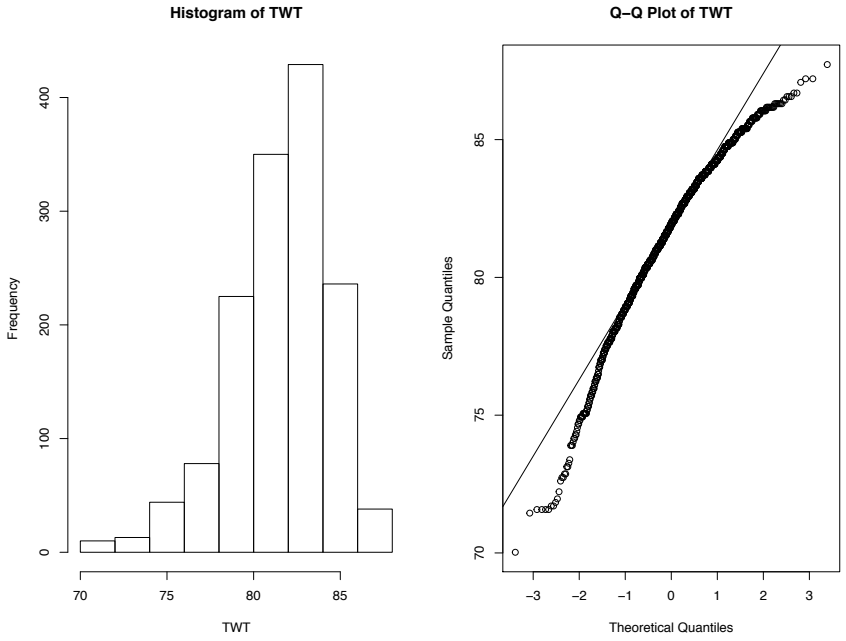



*Figure 2.15. Histogram and Q-Q Plot of Test Weight (TWT).*

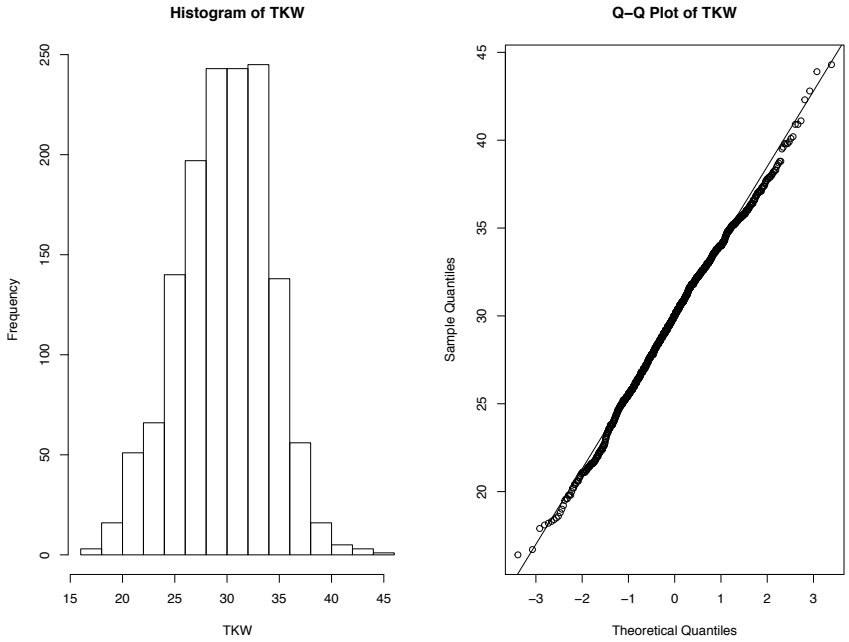



*Figure 2.16. Histogram and Q-Q Plot of Thousand Kernel Weight (TKW).*

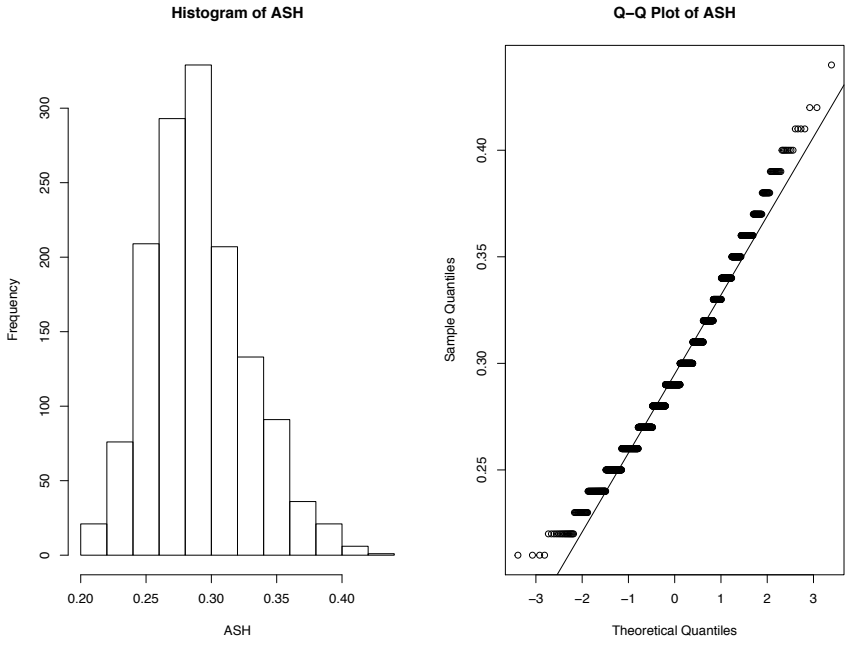



*Figure 2.17. Histogram and Q-Q Plot of Ash Content (ASH).*

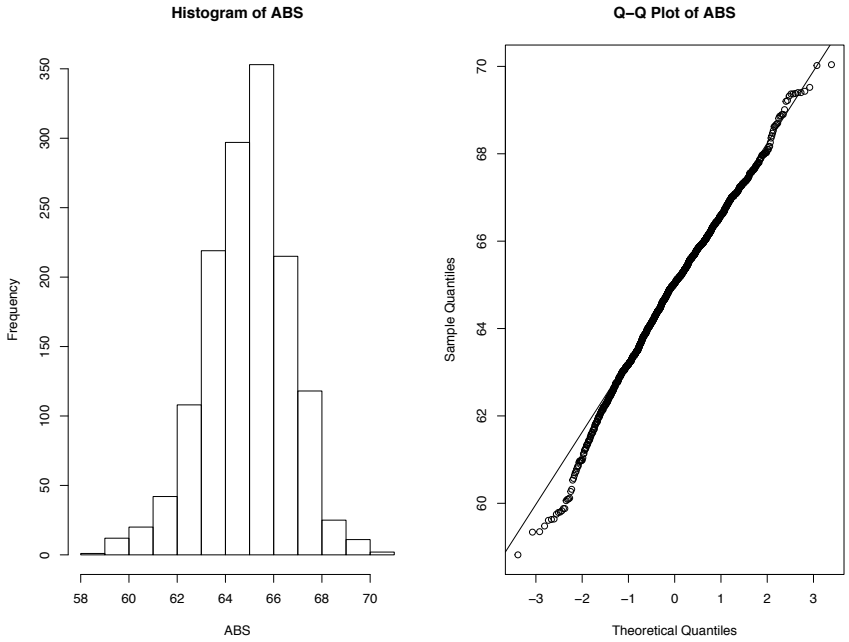



*Figure 2.18. Histogram and Q-Q Plot of Water Absorption (ABS).*

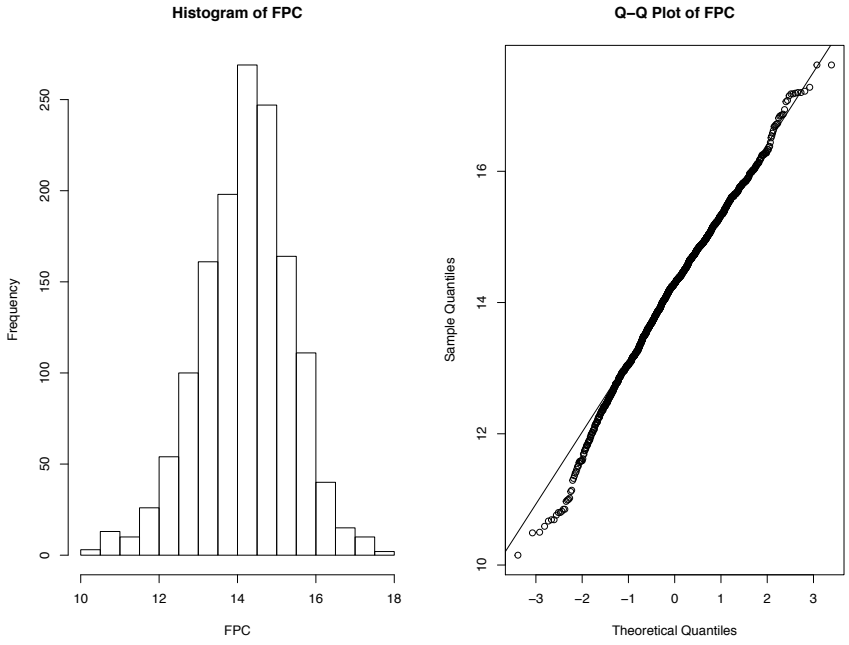



*Figure 2.19. Histogram and Q-Q Plot of Flour Protein Content (FPC).*

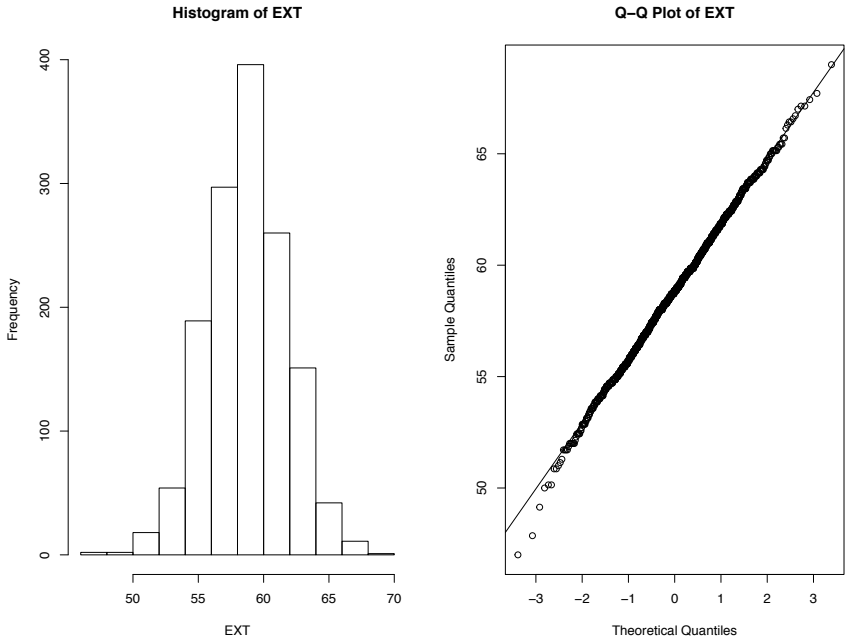



*Figure 2.20. Histogram and Q-Q Plot of Flour Extraction (EXT).*

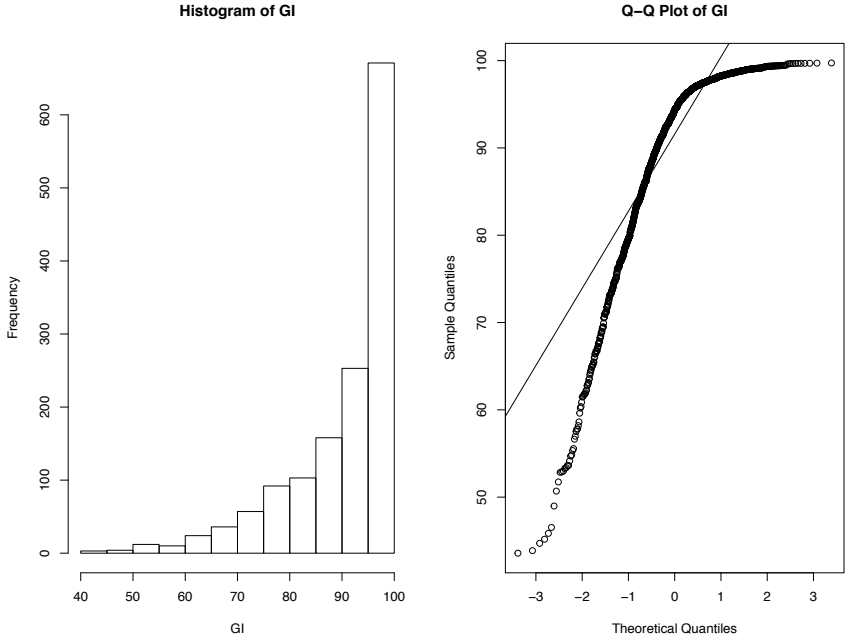



*Figure 2.21. Histogram and Q-Q Plot of Gluten Index (GI).*

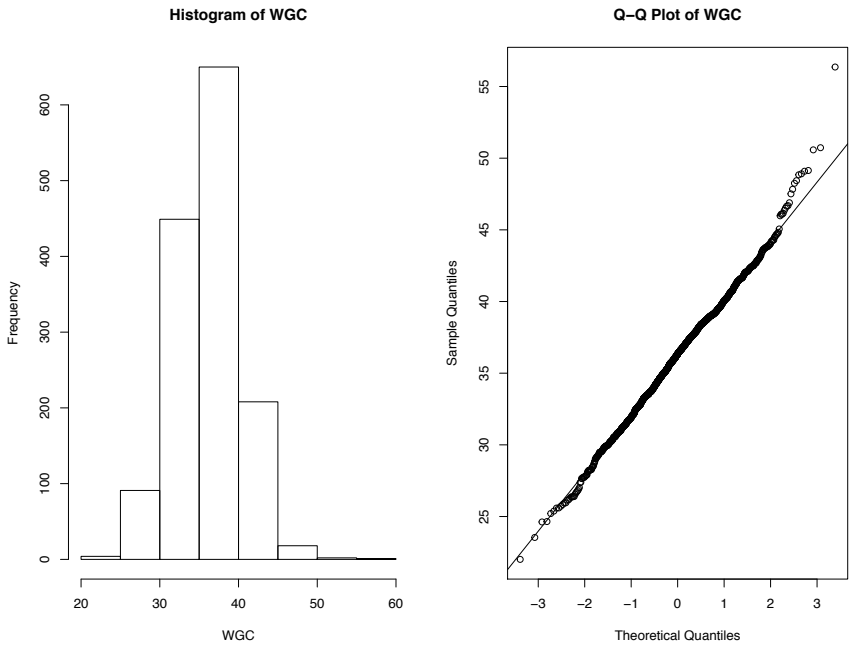



*Figure 2.22. Histogram and Q-Q Plot of Water Gluten Content (WGC).*

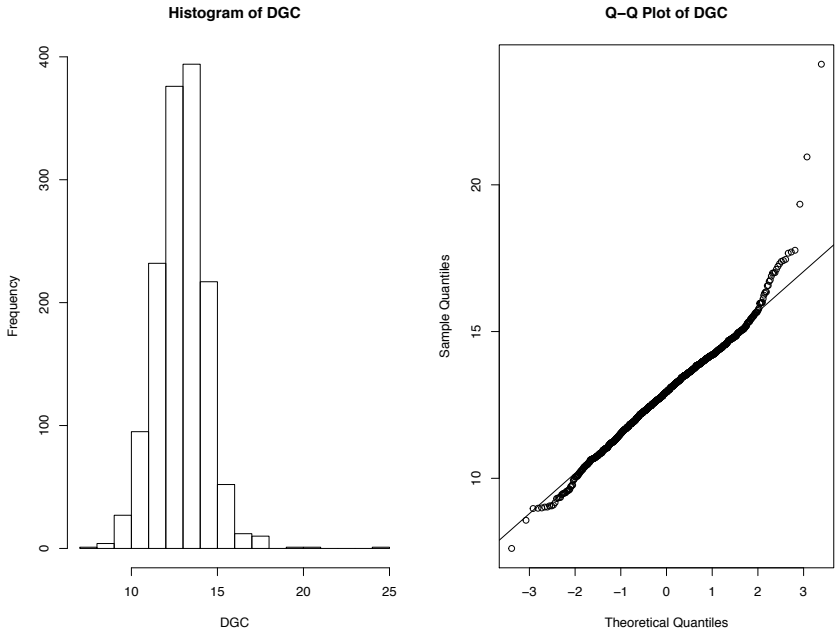



*Figure 2.23. Histogram and Q-Q Plot of Dry Gluten Content (DGC).*

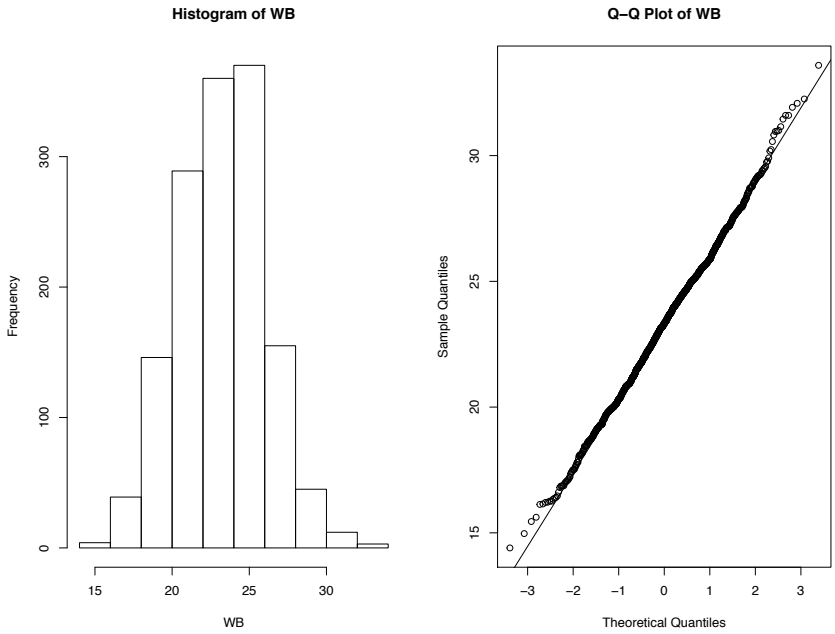



*Figure 2.24. Histogram and Q-Q Plot of Water-Binding (WB).*

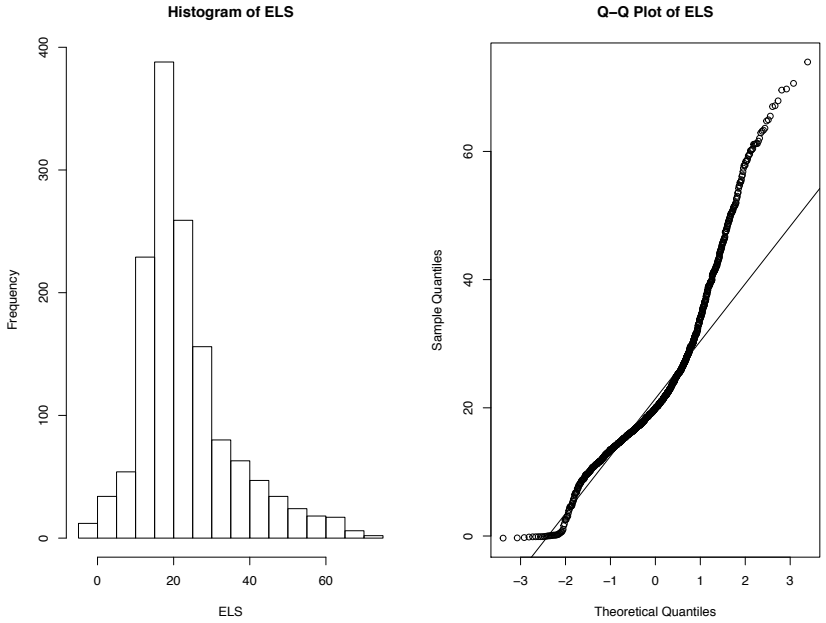



*Figure 2.25. Histogram and Q-Q Plot of Top-of-Envelope Left-of-Peak Slope (ELS).*

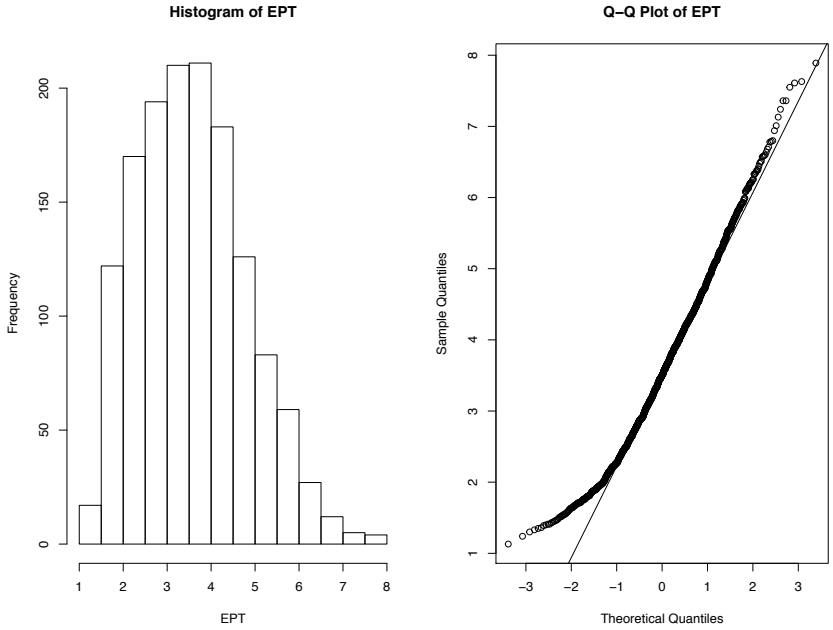



*Figure 2.26. Histogram and Q-Q Plot of Top-of-Envelope Peak Time (EPT).*

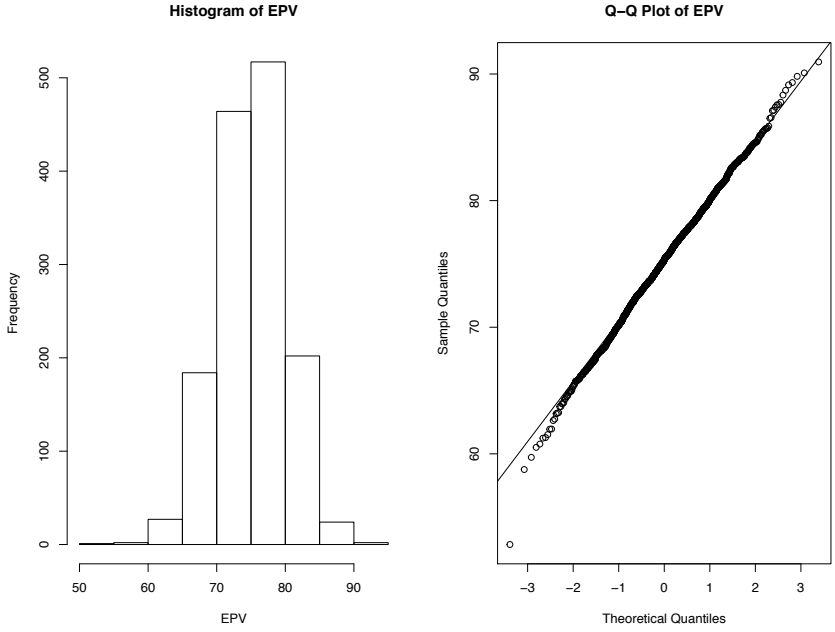



*Figure 2.27. Histogram and Q-Q Plot of Top-of-Envelope Peak Value (EPV).*

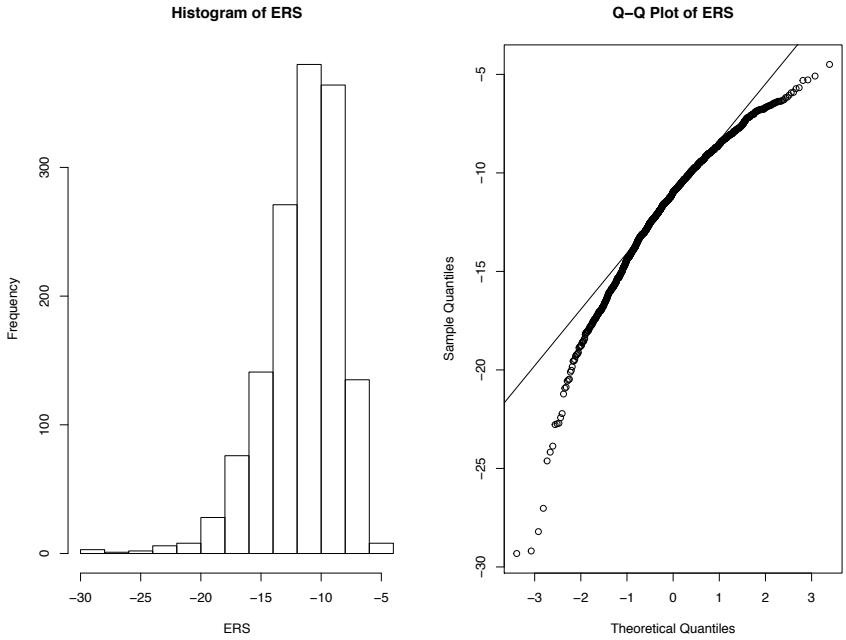



*Figure 2.28. Histogram and Q-Q Plot of Top-of-Envelope Right-of-Peak Slope (ERS).*

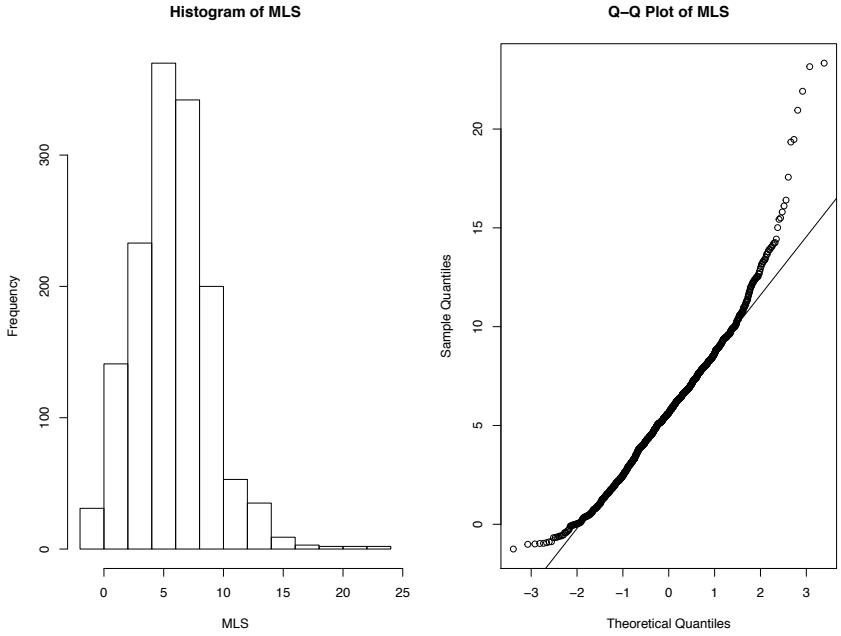



*Figure 2.29. Histogram and Q-Q Plot of Mid-Line Left-of-Peak Slope (MLS).*

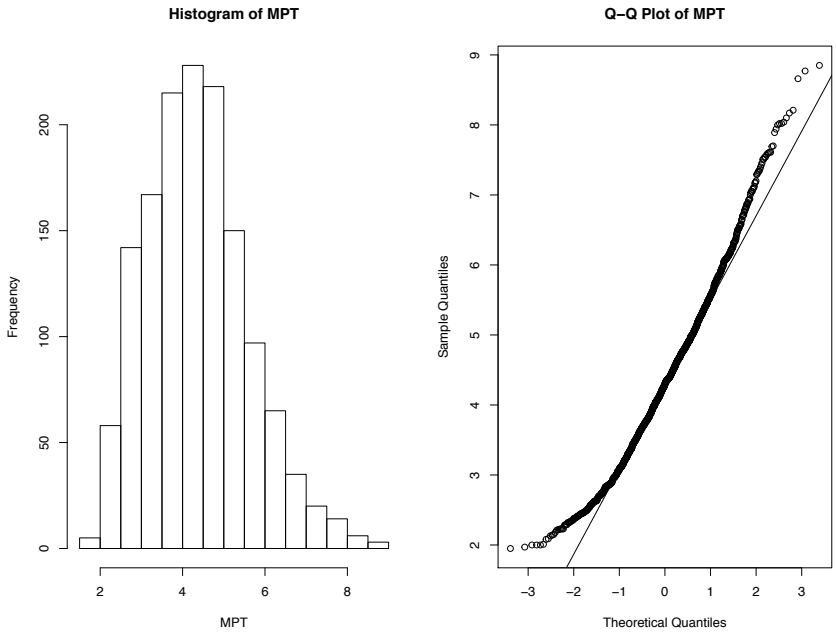



*Figure 2.30. Histogram and Q-Q Plot of Mid-Line Peak Time (MPT).*

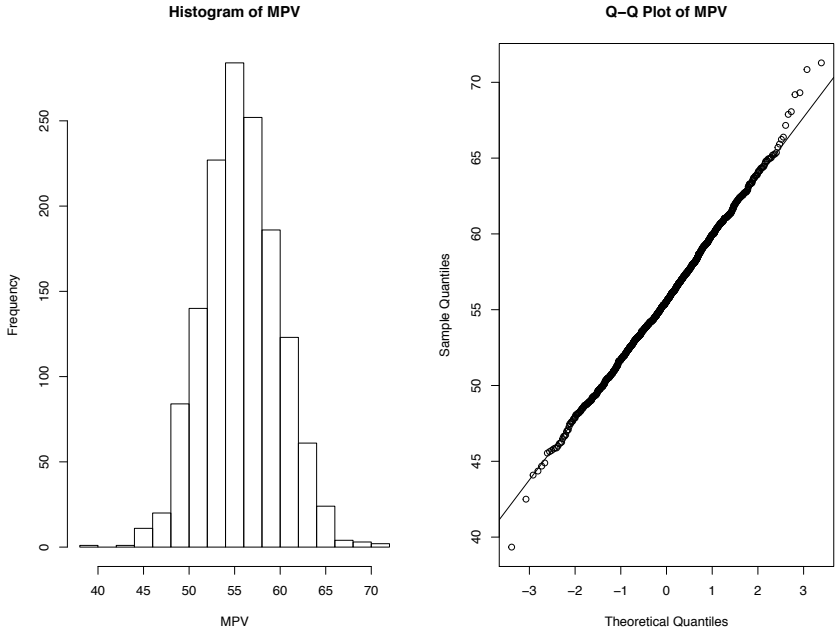



*Figure 2.31. Histogram and Q-Q Plot of Mid-Line Peak Value (MPV).*

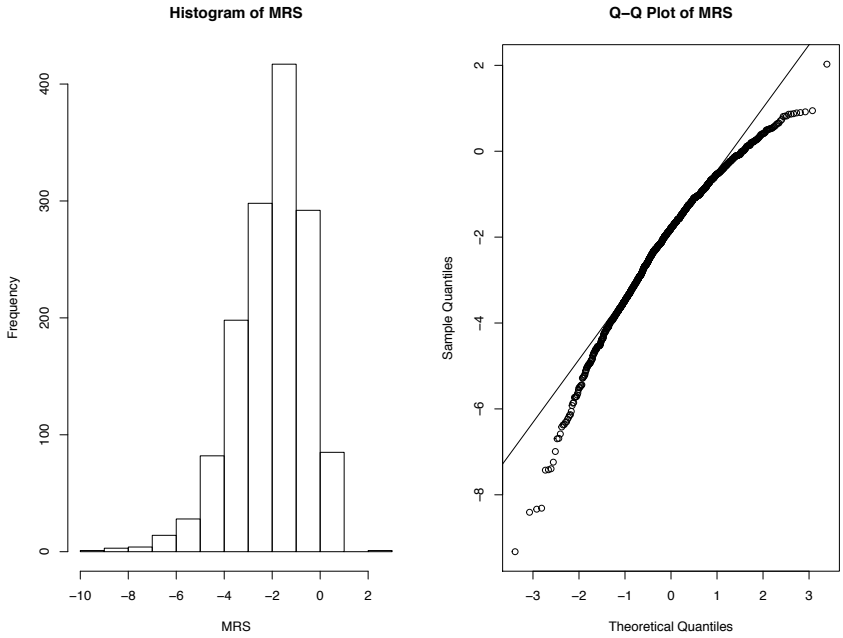



*Figure 2.32. Histogram and Q-Q Plot of Mid-Line Right-of-Peak Slope (MRS).*

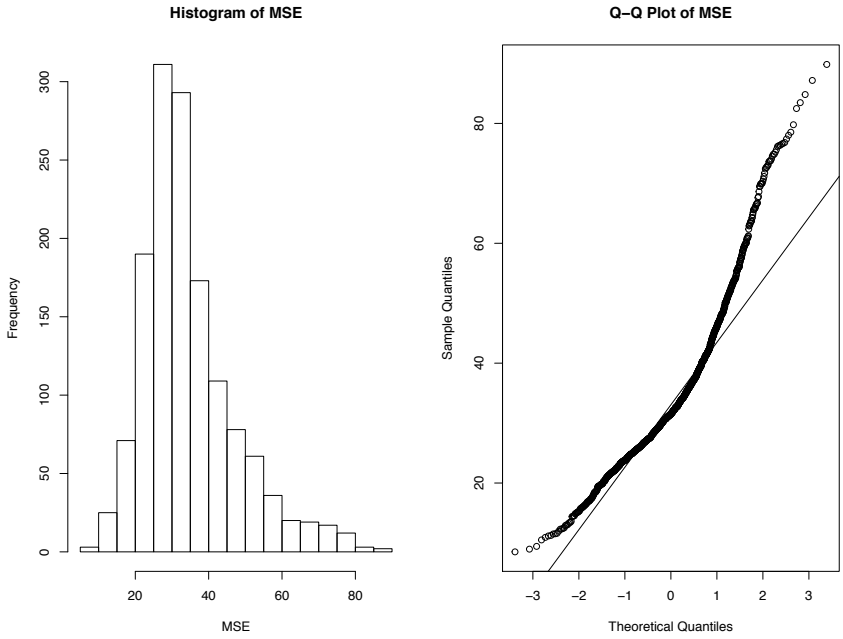



*Figure 2.33. Histogram and Q-Q Plot of Top-of-Envelope Mixing Stability (MSE).*

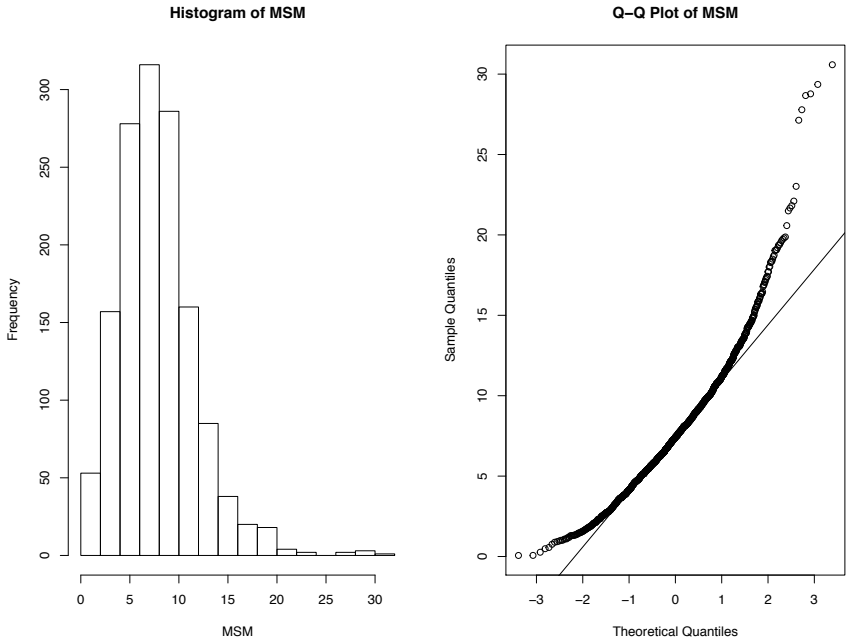



*Figure 2.34. Histogram and Q-Q Plot of Mid-Line Mixing Stability (MSM).*

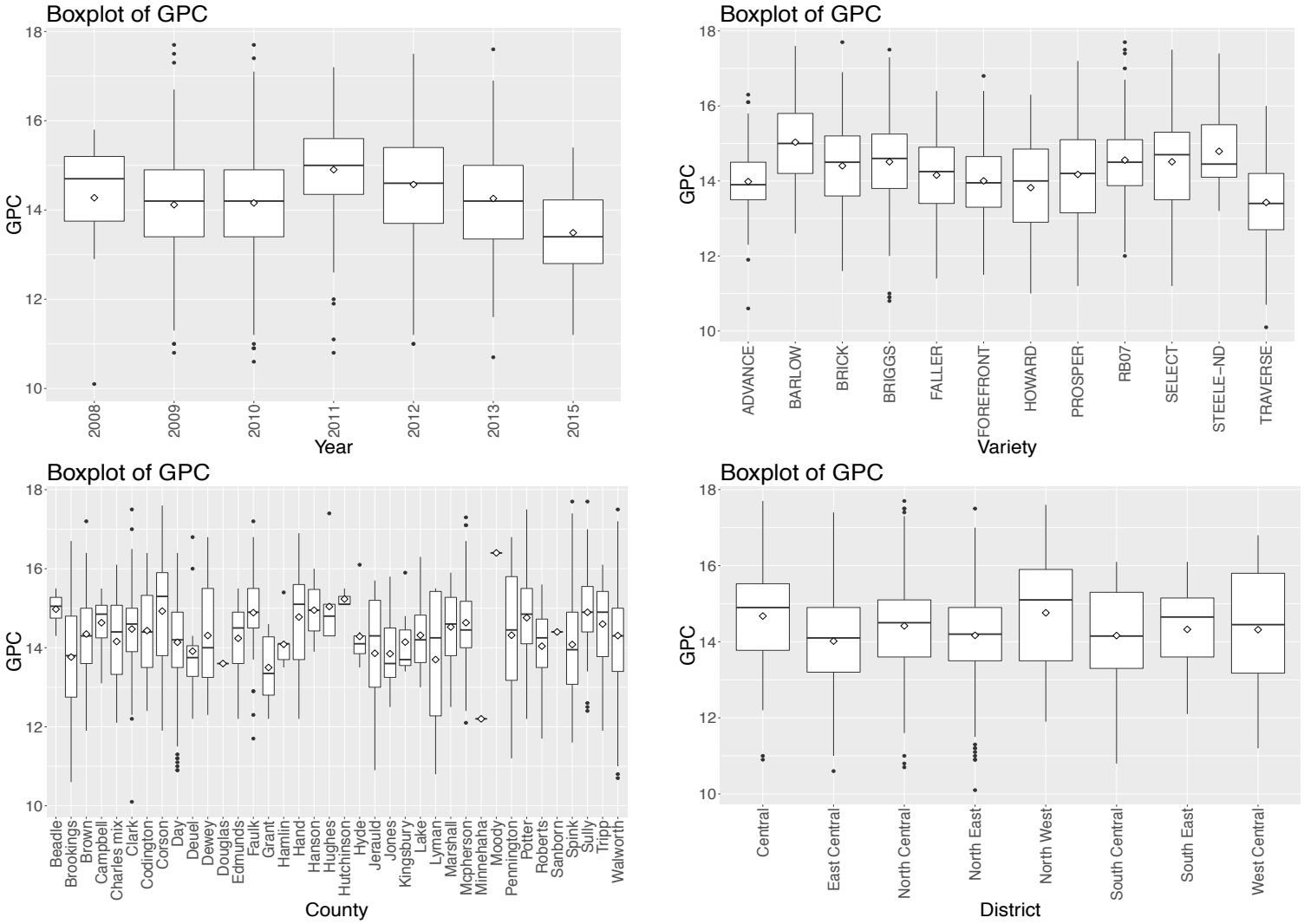



*Figure 2.35. Boxplots of Year, Variety, County, and District for Grain Protein Content (GPC).*

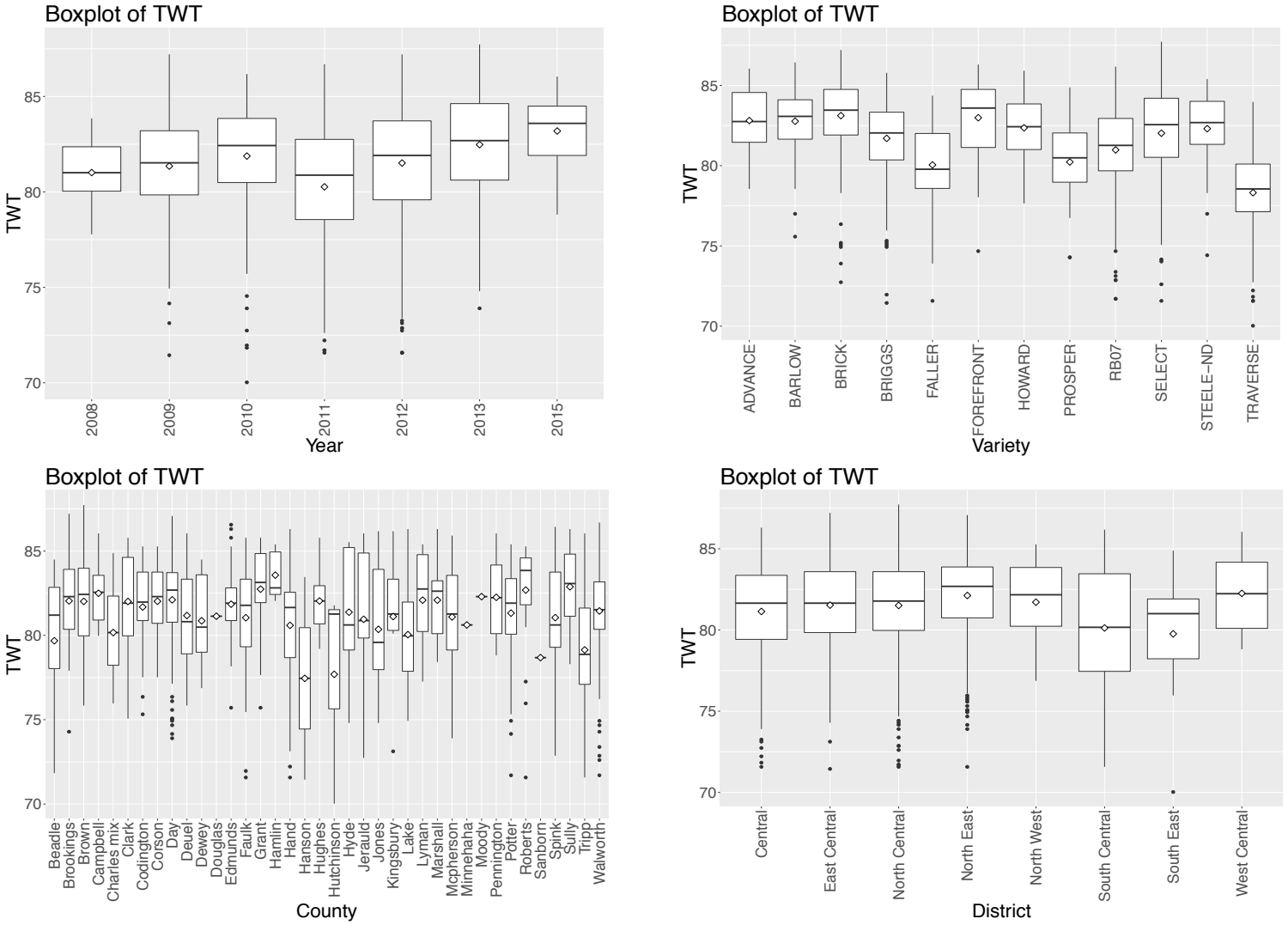



*Figure 2.36. Boxplots of Year, Variety, County, and District for Test Weight (TWT).*

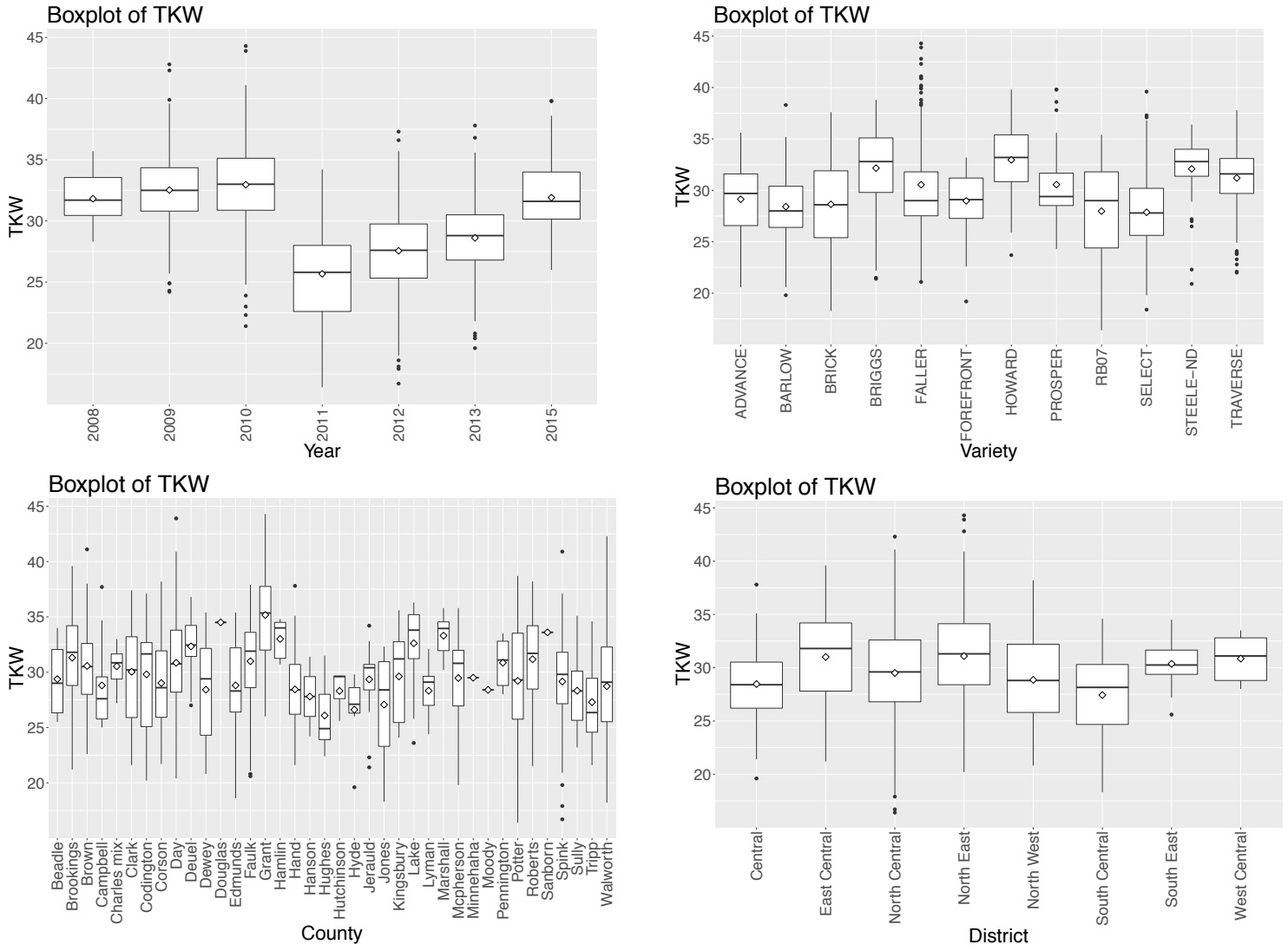



*Figure 2.37. Boxplots of Year, Variety, County, and District for Thousand Kernel Weight (TKW).*

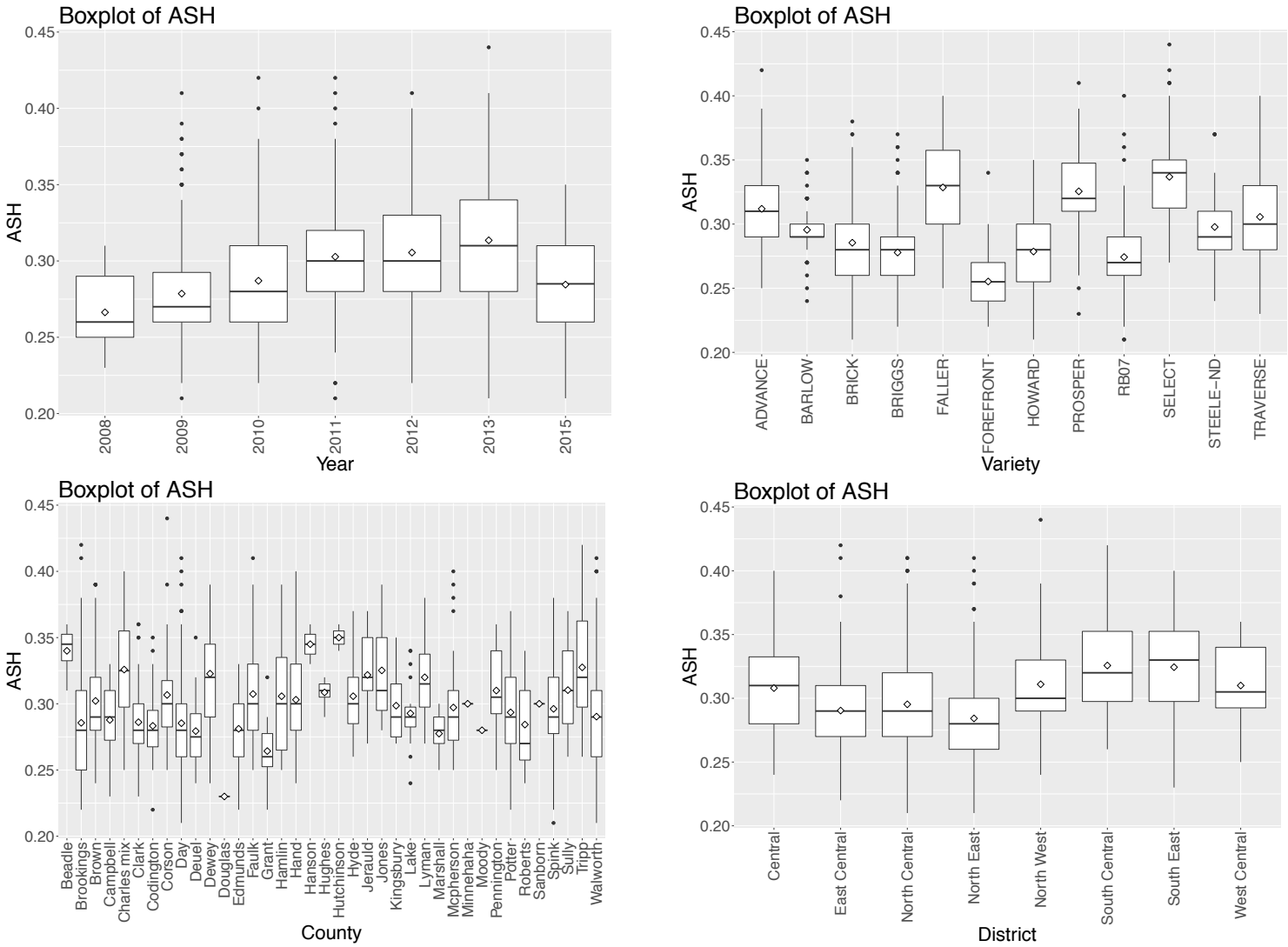



*Figure 2.38. Boxplots of Year, Variety, County, and District for Ash Content (ASH).*

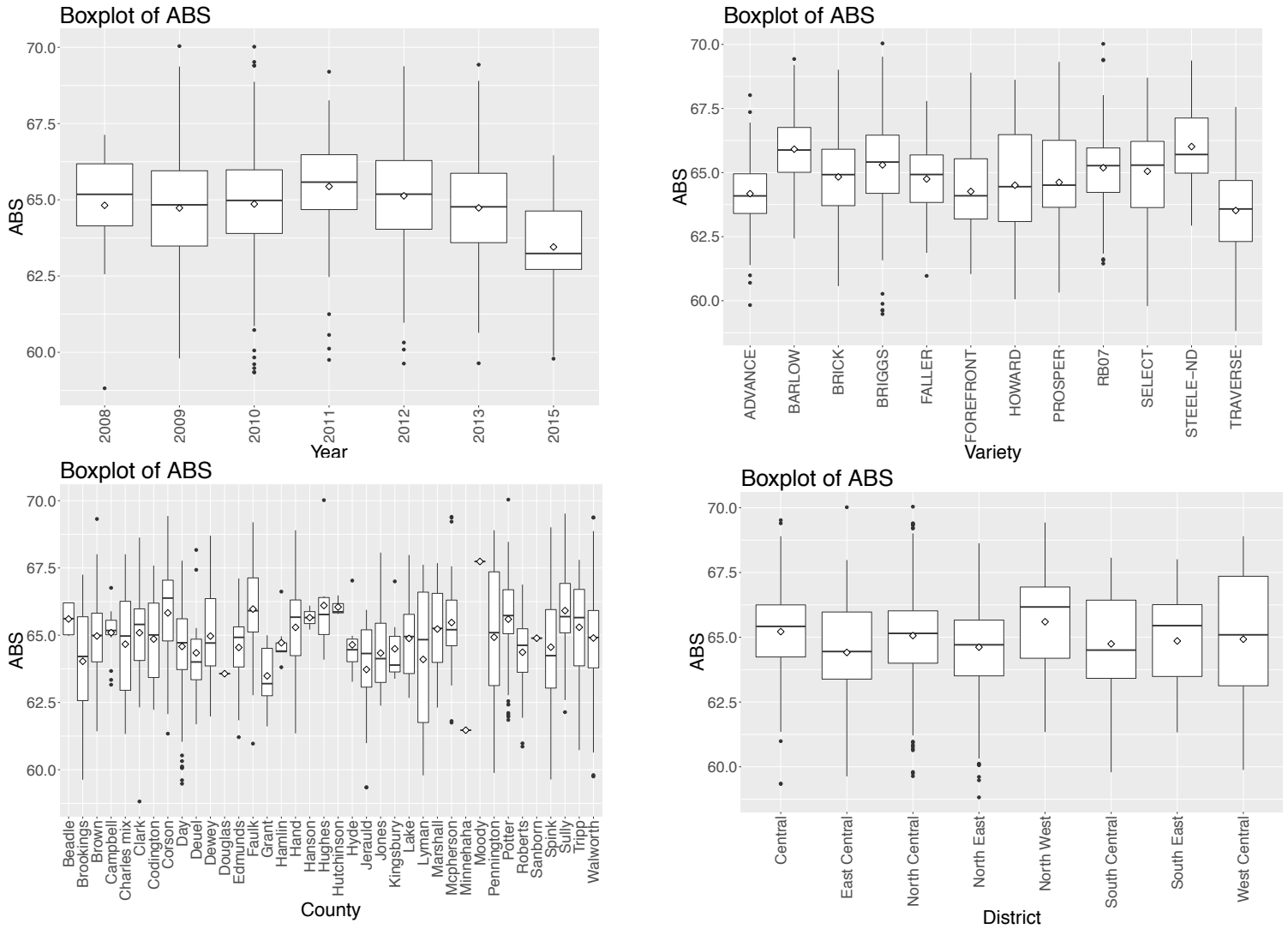



*Figure 2.39. Boxplots of Year, Variety, County, and District for Water Absorption (ABS).*

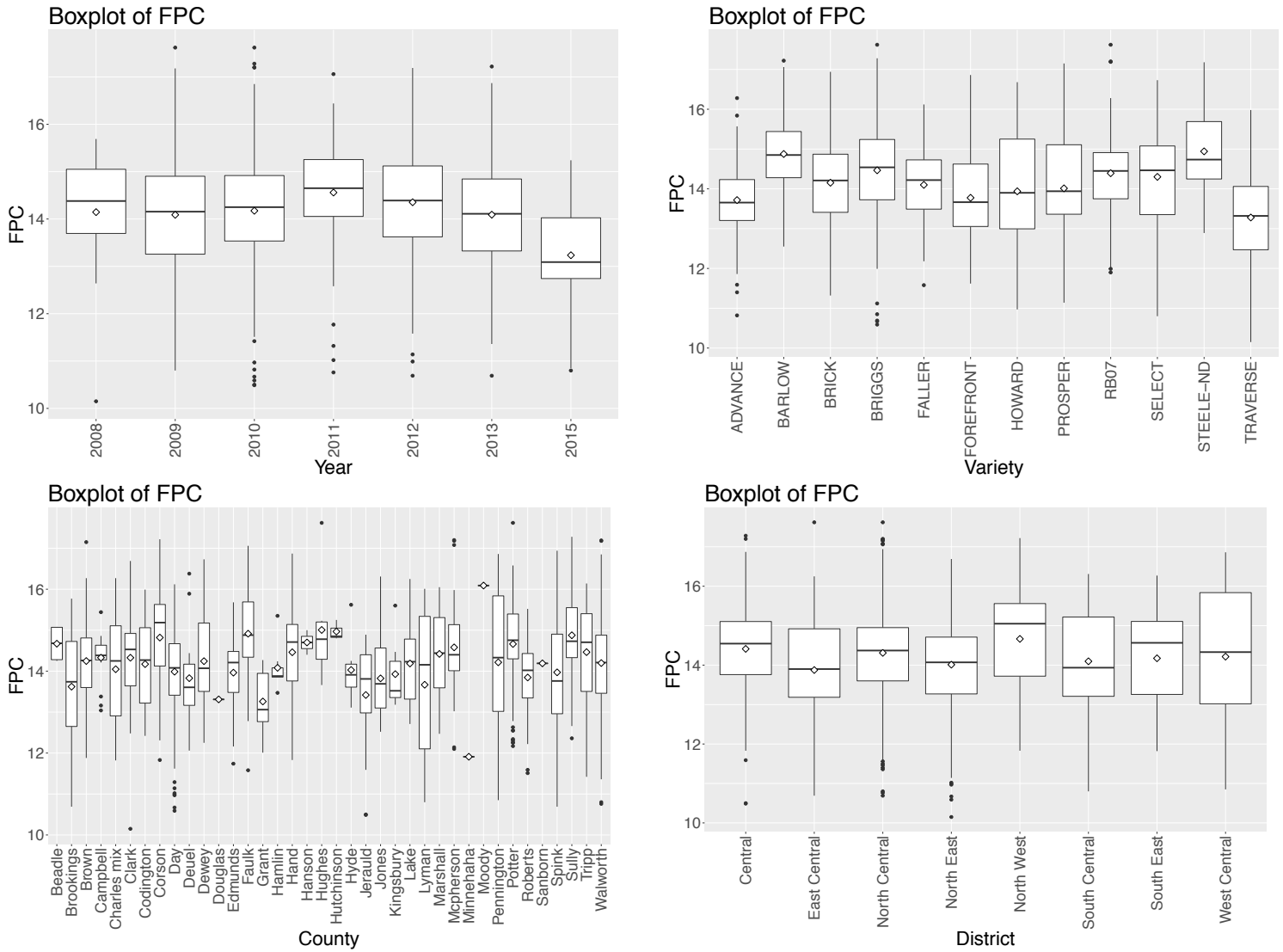



*Figure 2.40. Boxplots of Year, Variety, County, and District for Flour Protein Content (FPC).*

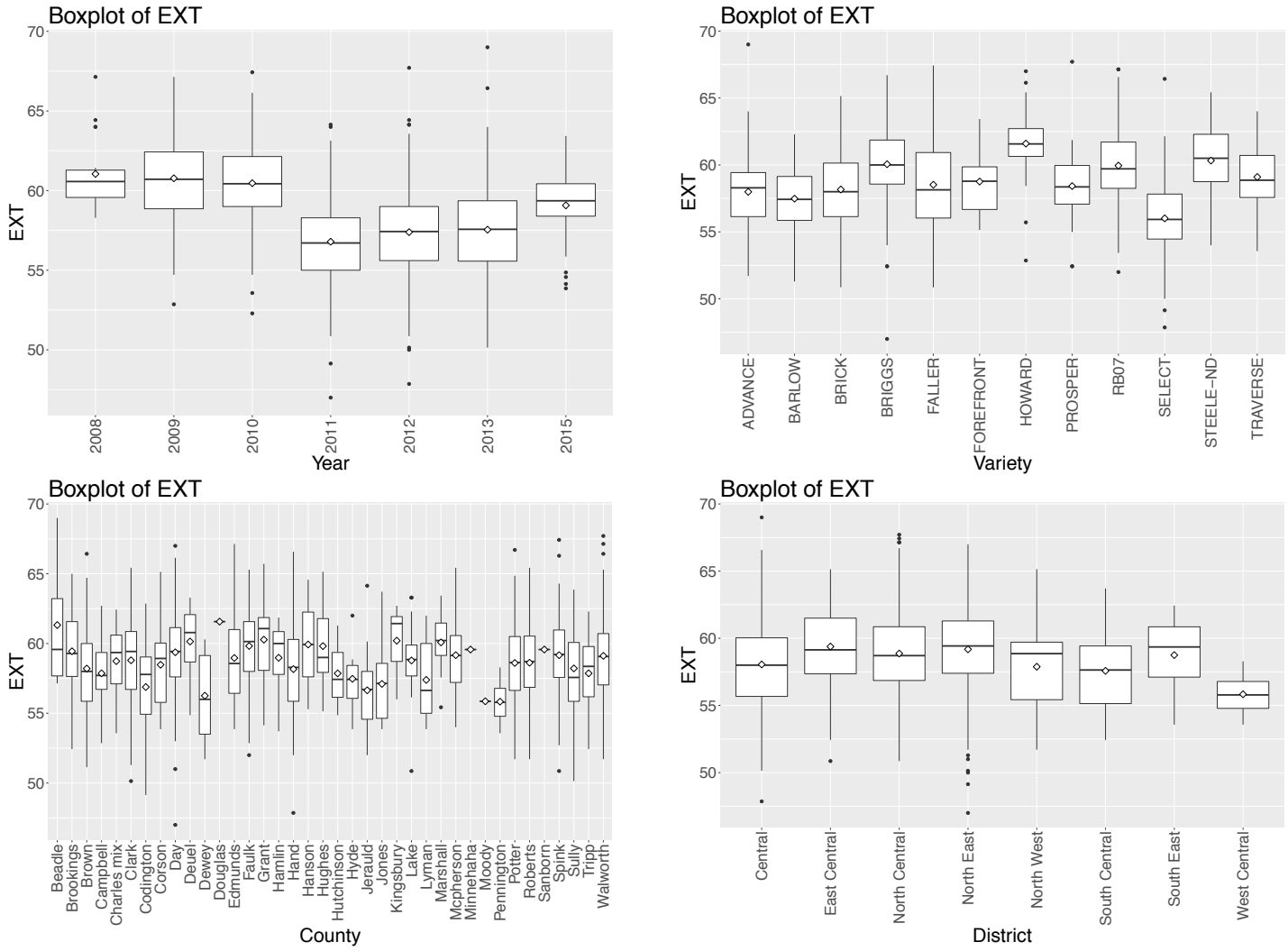



*Figure 2.41. Boxplots of Year, Variety, County, and District for Flour Extraction (EXT).*

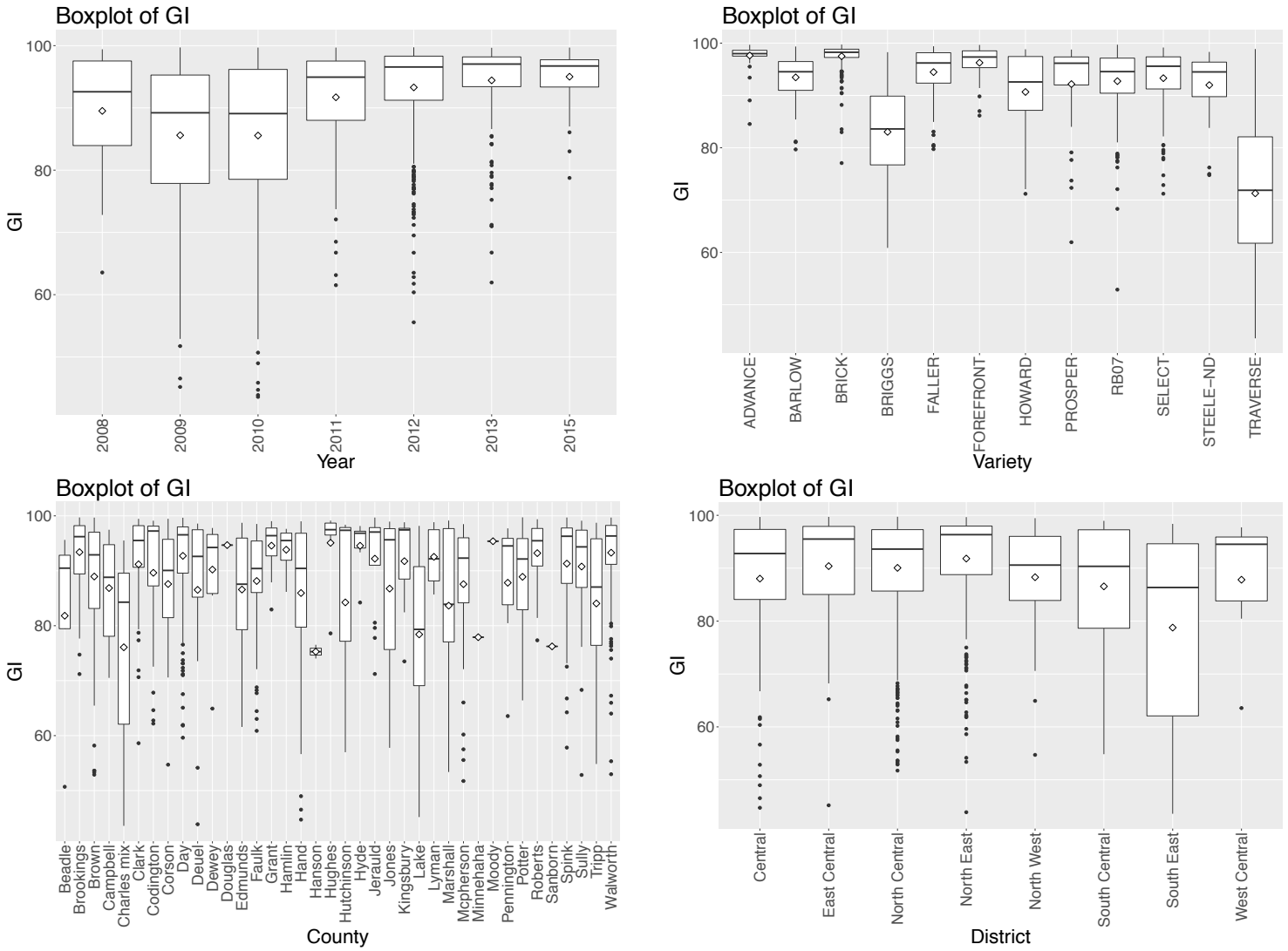



*Figure 2.42. Boxplots of Year, Variety, County, and District for Gluten Index (GI).*

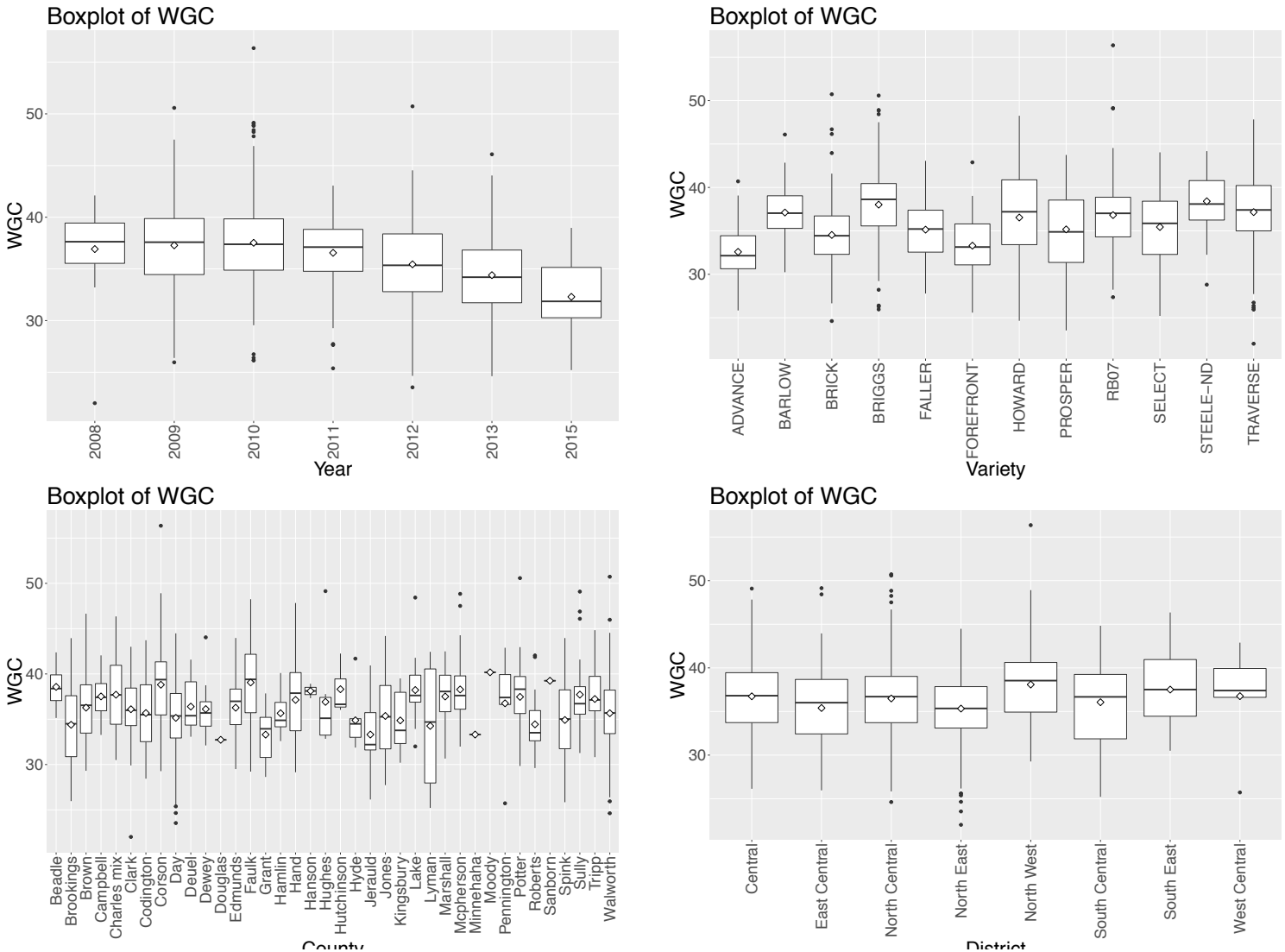



*Figure 2.43. Boxplots of Year, Variety, County, and District for Wet Gluten Content (WGC).*

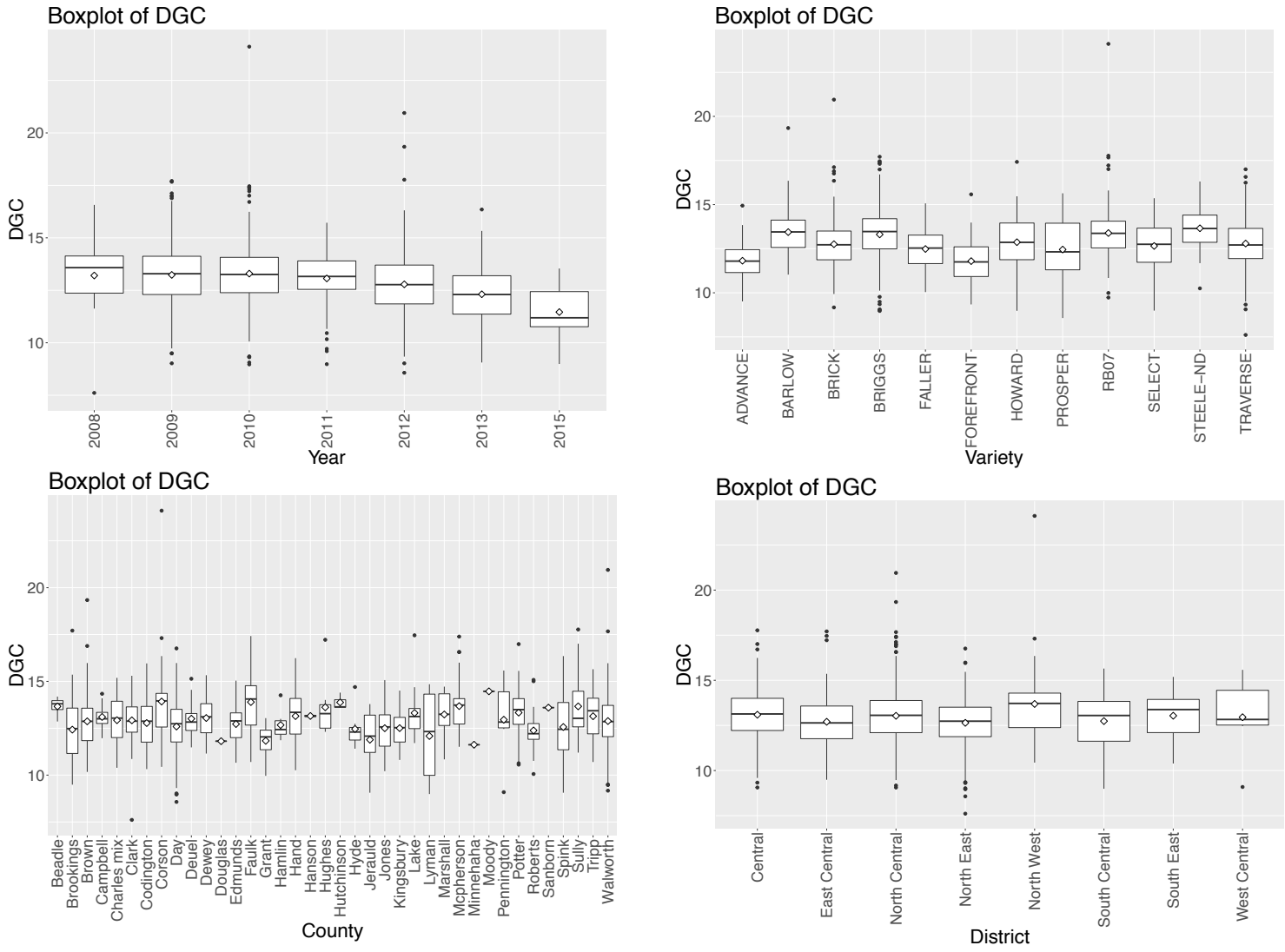



*Figure 2.44. Boxplots of Year, Variety, County, and District for Dry Gluten Content (DGC).*

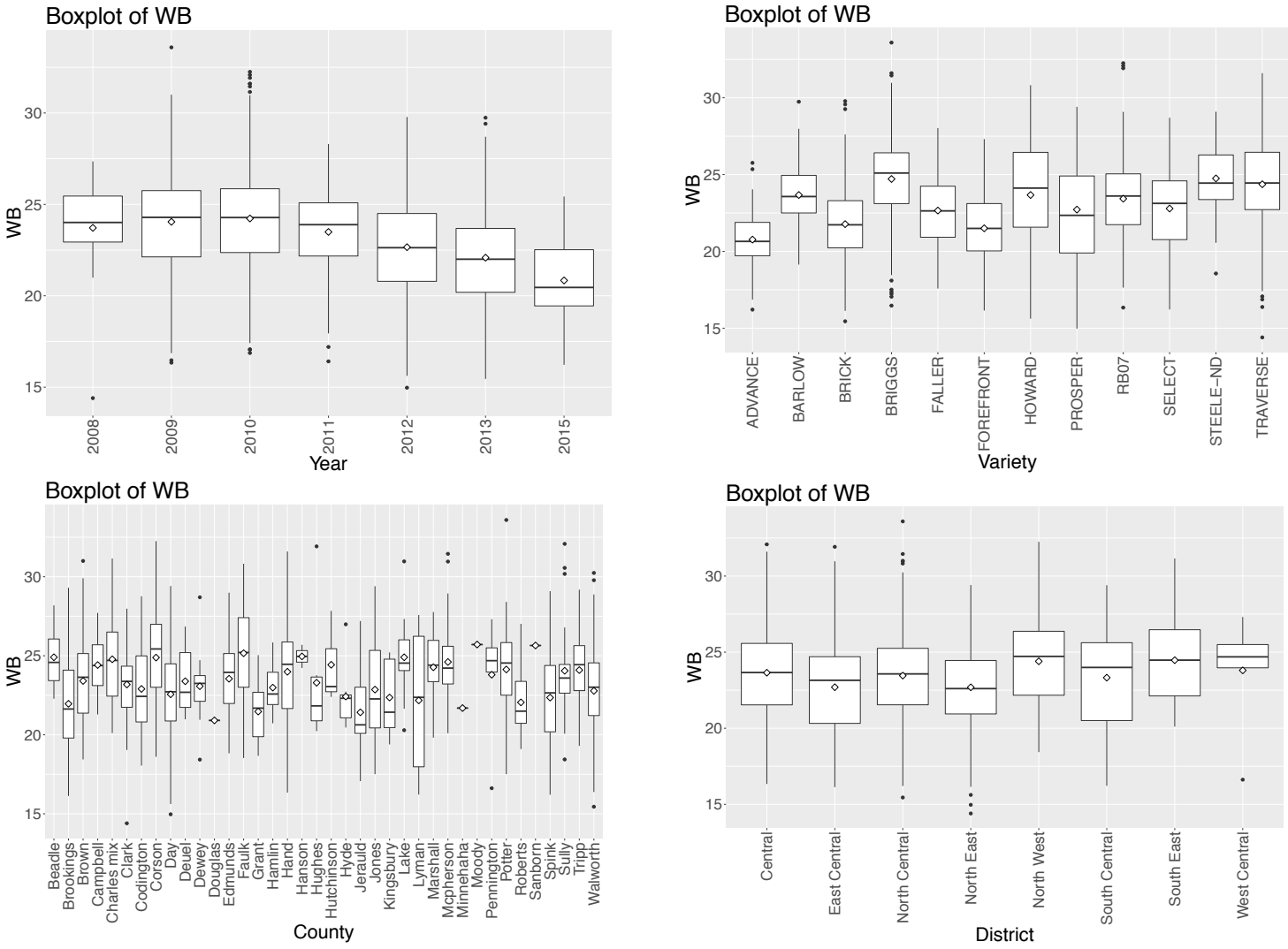



*Figure 2.45. Boxplots of Year, Variety, County, and District for Water-Binding (WB).*

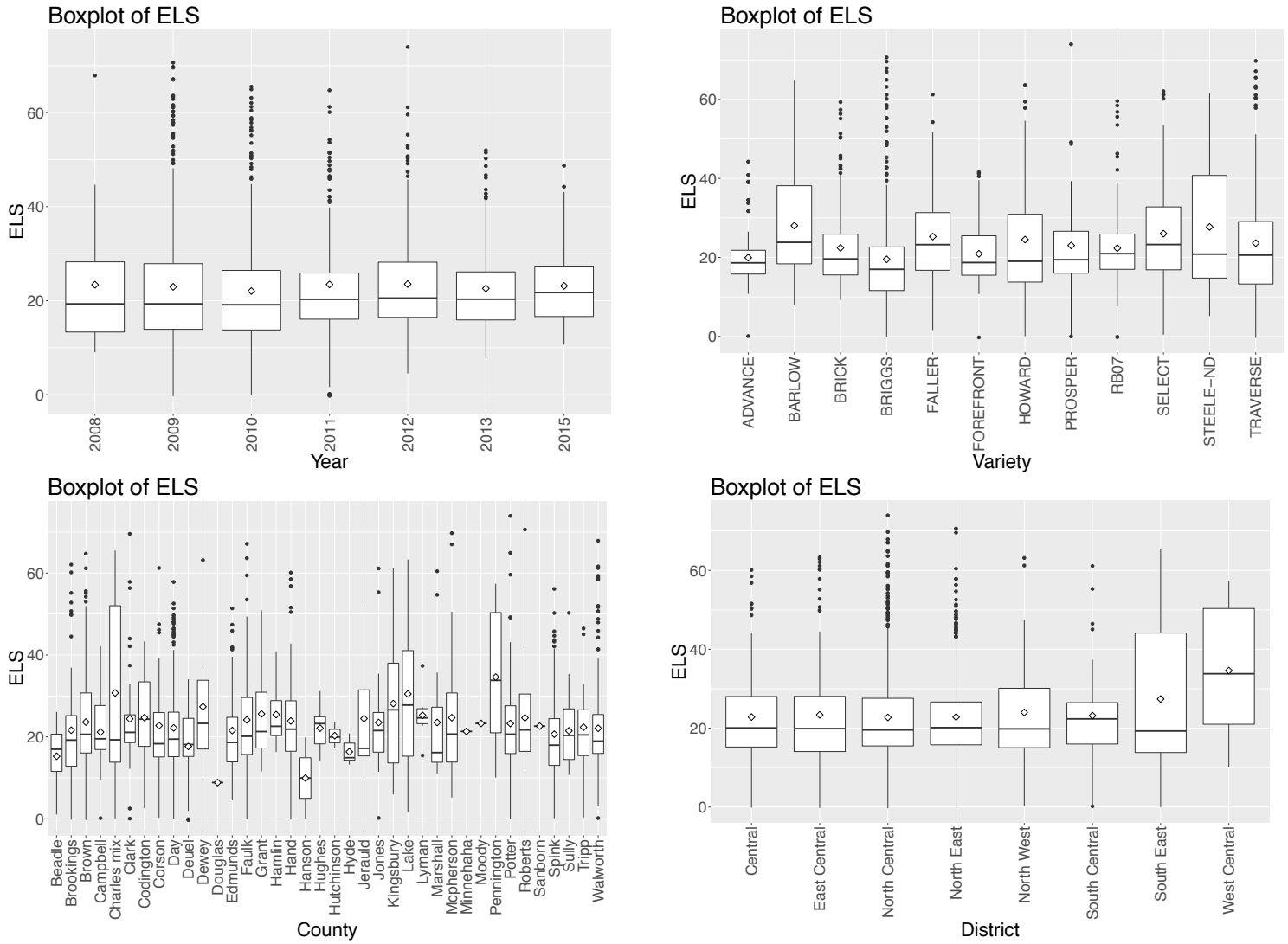



*Figure 2.46. Boxplots of Year, Variety, County, and District for Top-of-Envelope Left-of-Peak Slope (ELS).*

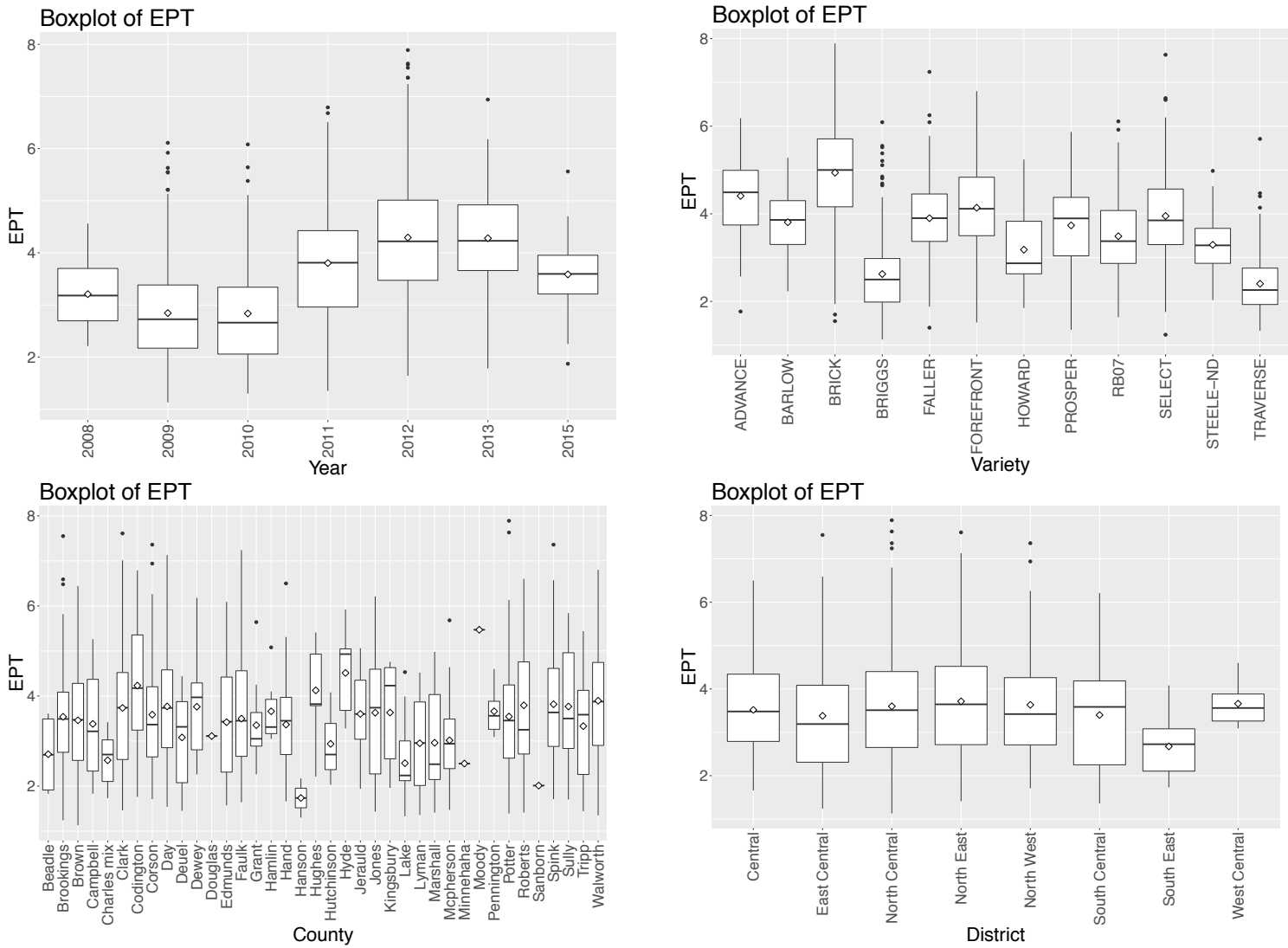



*Figure 2.47. Boxplots of Year, Variety, County, and District for Top-of-Envelope Peak Time (EPT).*

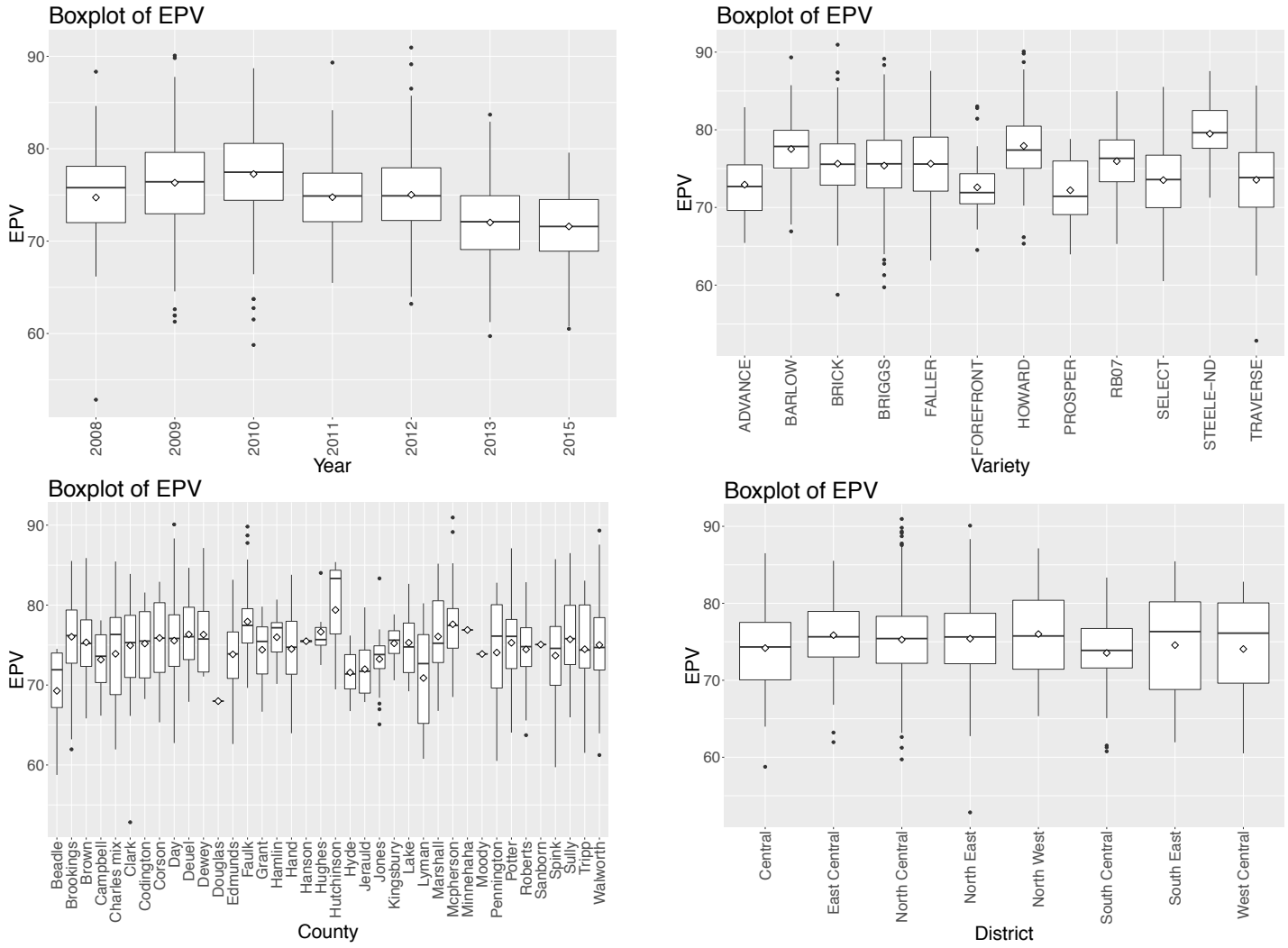



*Figure 2.48. Boxplots of Year, Variety, County, and District for Top-of-Envelope Peak Value (EPV).*

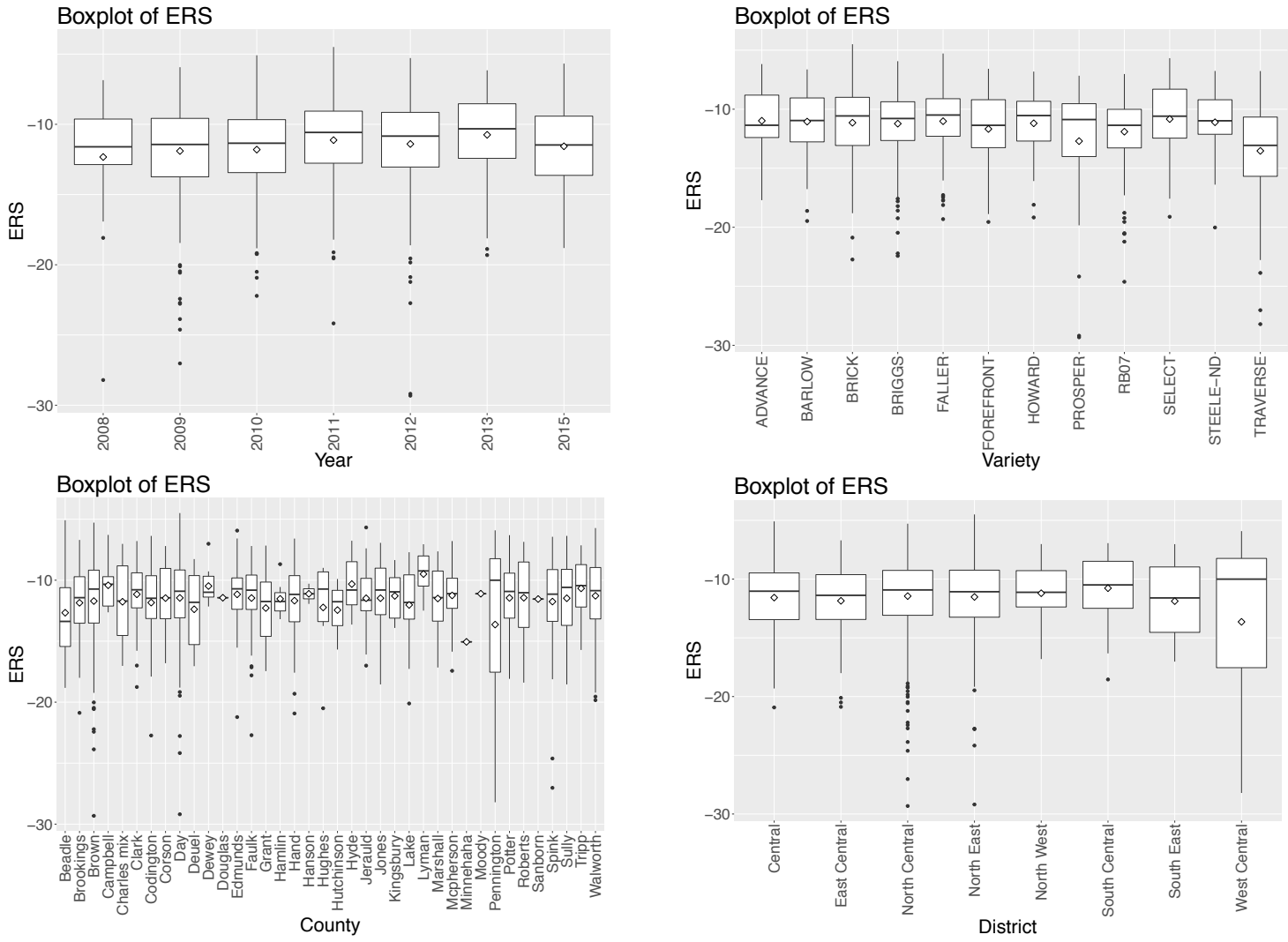



*Figure 2.49. Boxplots of Year, Variety, County, and District for Top-of-Envelope Right-of-Peak Slope (ERS).*

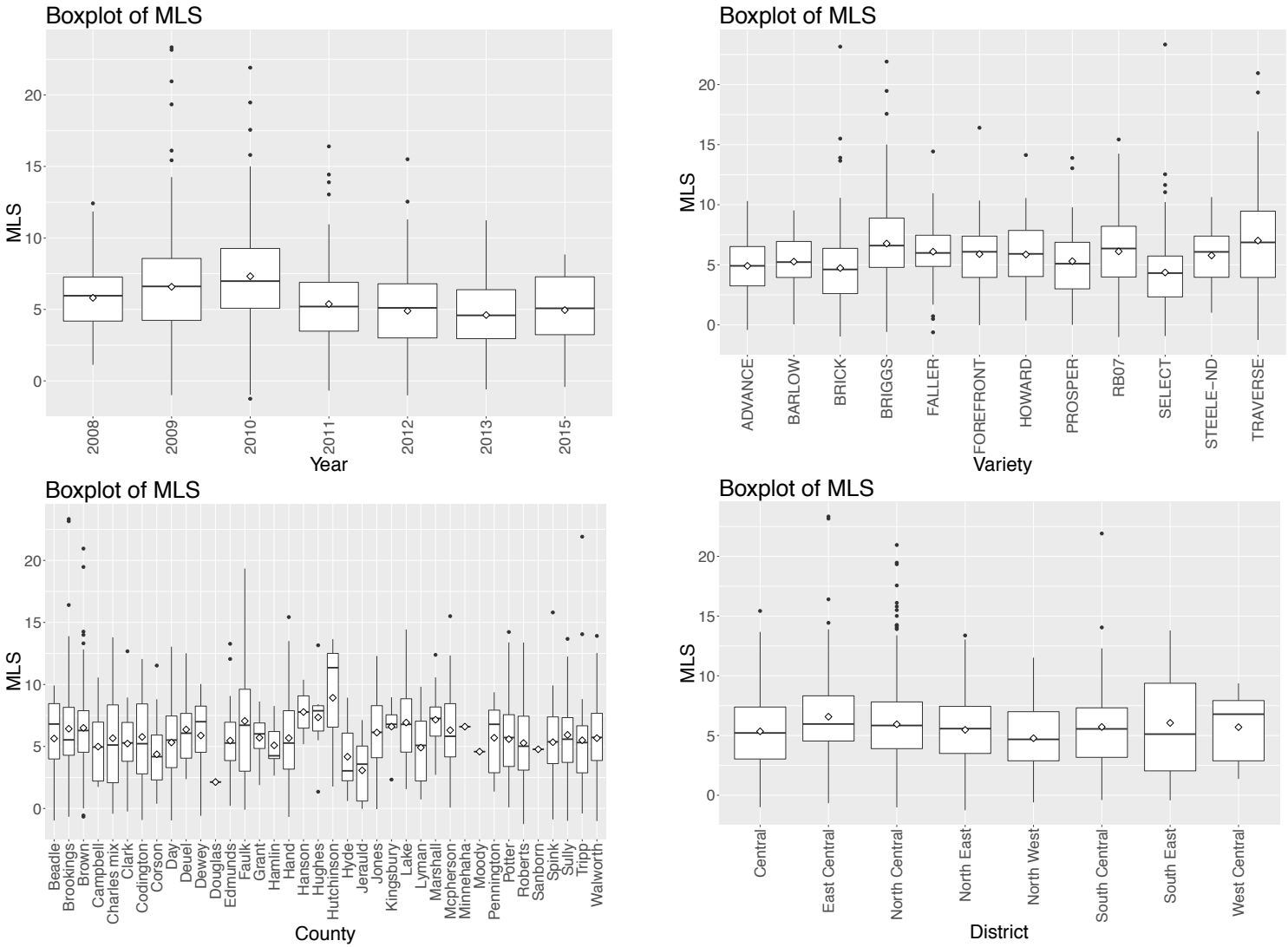



*Figure 2.50. Boxplots of Year, Variety, County, and District for Mid-Line Left-of-Peak Slope (MLS).*

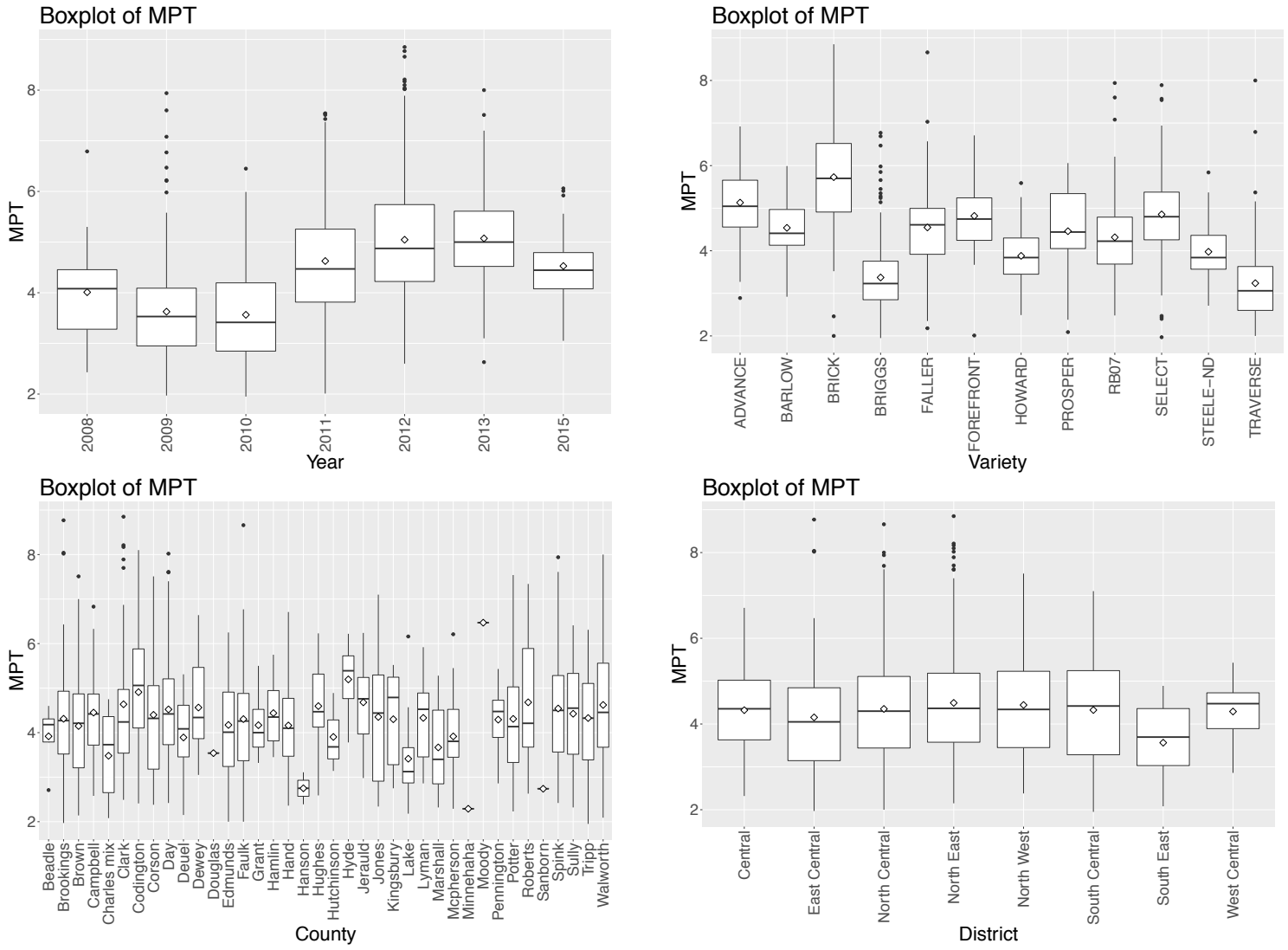



*Figure 2.51. Boxplots of Year, Variety, County, and District for Mid-Line Peak Time (MPT).*

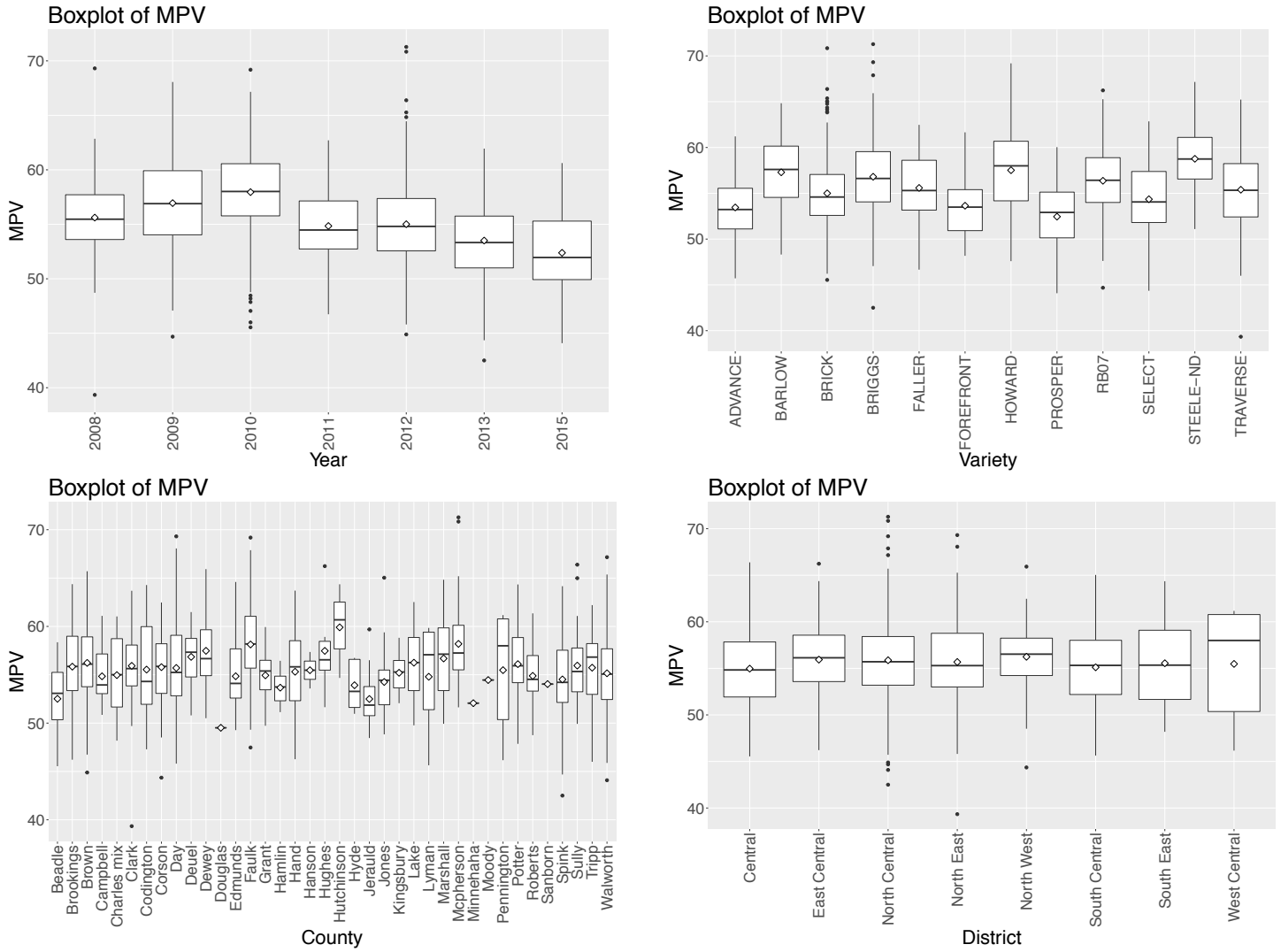



*Figure 2.52. Boxplots of Year, Variety, County, and District for Mid-Line Peak Value (MPV).*

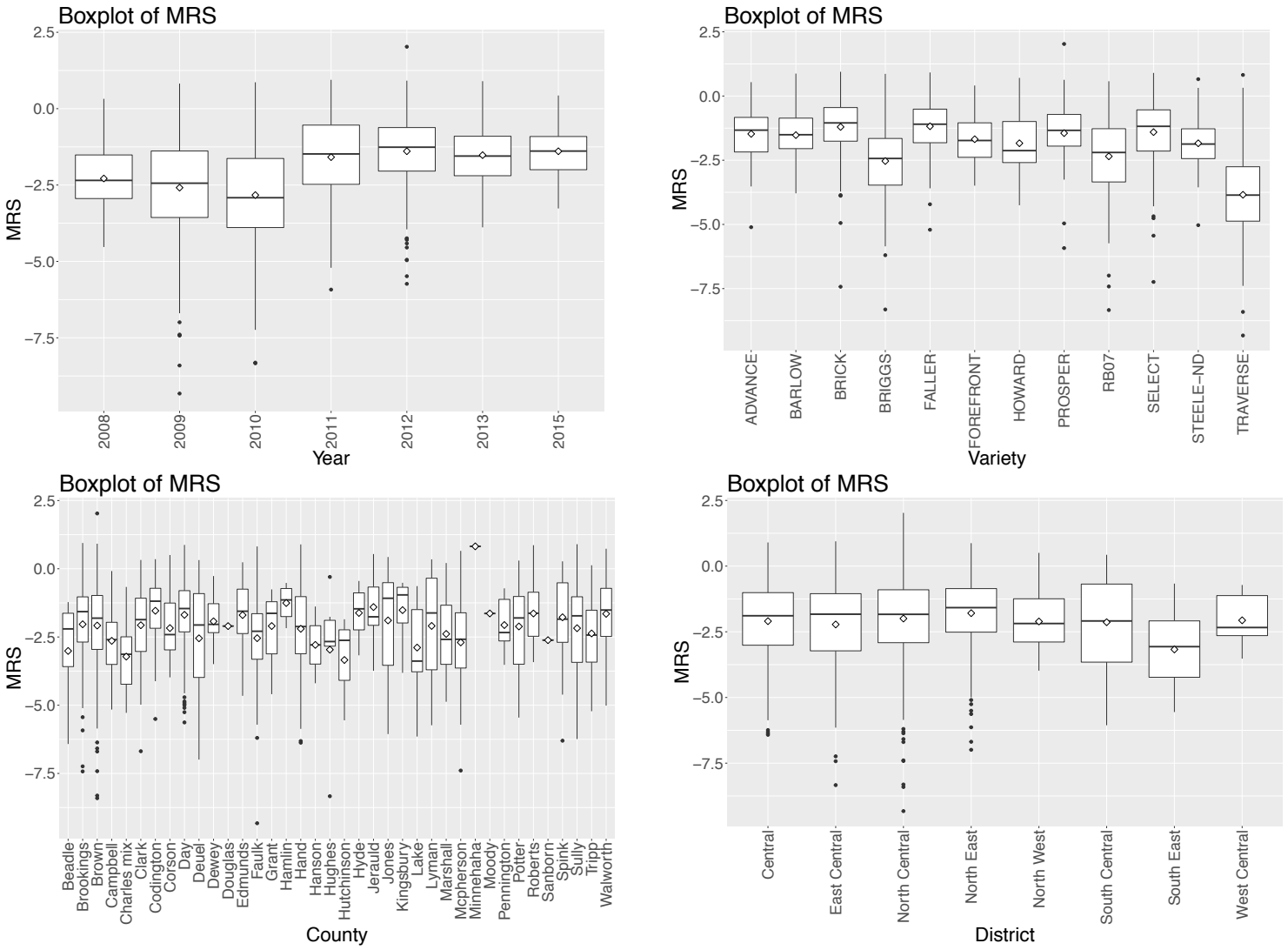



*Figure 2.53. Boxplots of Year, Variety, County, and District for Mid-Line Right-of-Peak Slope (MRS).*

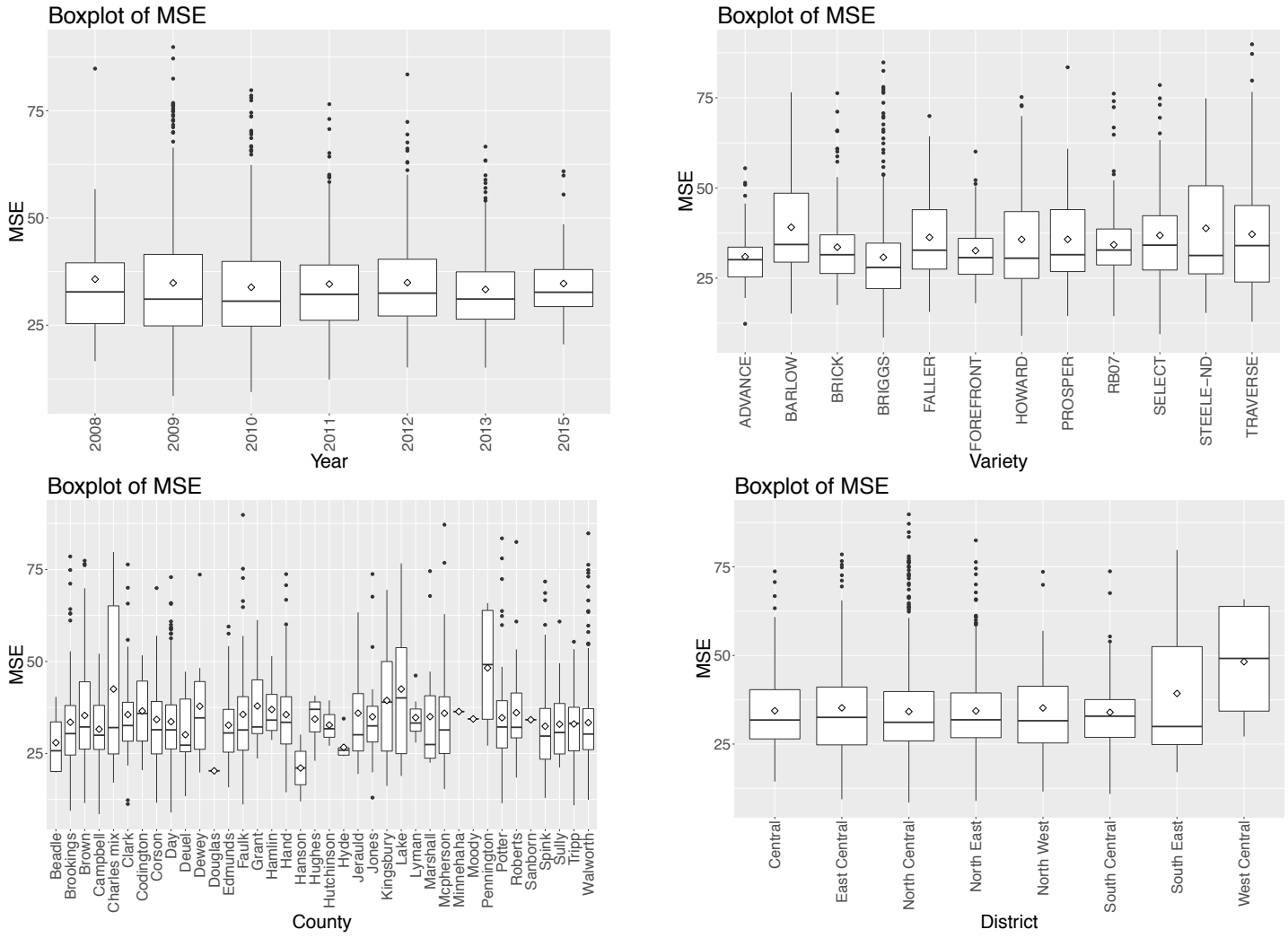



*Figure 2.54. Boxplots of Year, Variety, County, and District for Top-of-Envelope Mixing Stability (MSE).*

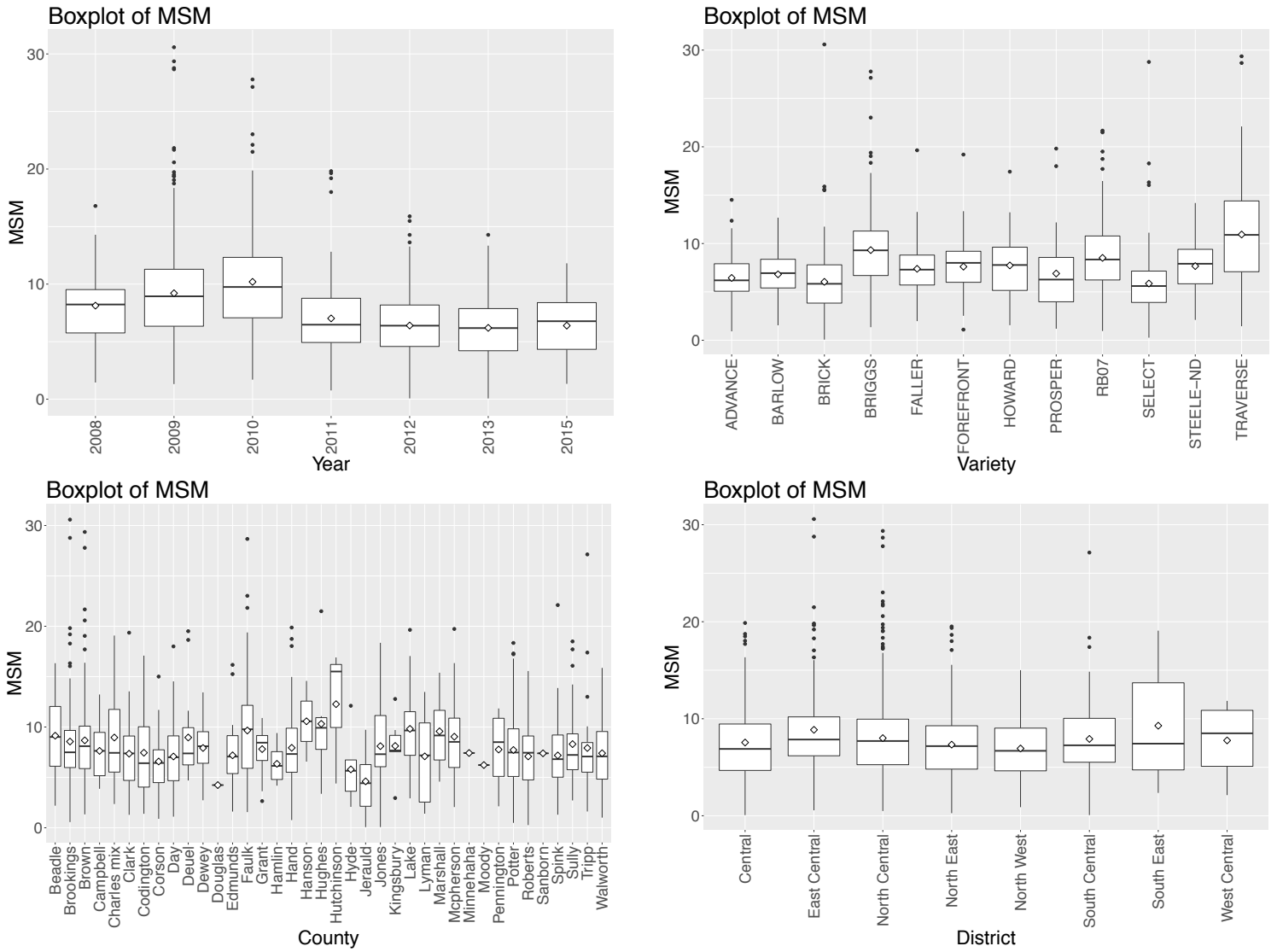



*Figure 2.55. Boxplots of Year, Variety, County, and District for Mid-Line Mixing Stability (MSM).*

# CHAPTER 3: GGE AND BIPLOT ANALYSIS OF QUALITY TRAITS IN HARD RED SPRING WHEAT GROWN IN SOUTH DAKOTA

## ABSTRACT

Determining how production years and locations influenced end-use quality traits will assist breeders, agronomists, and growers, in understanding which hard red spring wheat (HRSW; *Triticum aestivum* L.) varieties are least susceptible to quality fluctuations, and therefore, most desirable to end-users. In order to determine which varieties were more consistent in certain locations, evaluations on how end-use quality fluctuates in specific locations was conducted. Analyses were completed on an unbalanced dataset represented by one thousand four hundred and twenty-three HRSW samples from seven years and thirty-eight counties throughout South Dakota comprised of twelve varieties.

To overcome the analytical challenges with incomplete datasets, Pearson correlation coefficients, variance component estimation and heritability using a genotype-by-location-by year (GLY) linear mixed model, along with biplot analysis for mega-environment evaluation using singular value decomposition (SVD) analysis was completed for 21 end-use quality traits.

Predicted estimates from the adjusted unbiased prediction approach (AUP) and biplot analysis, determined that Briggs, Steele-ND, and Barlow varieties resulted in the best end-use quality wheat for most of the counties represented in South Dakota. This study also revealed the higher end-use quality, in regard to protein, gluten, and

rheological traits, effect for Faulk, Beadle, and Hutchinson counties. The results of the combination of biplots and variance component estimation is that traits are more variable between years and varieties as compared to the counties. This indicates that specific county effects are not large enough to ignore the importance of selecting the proper variety and testing it in multiple years.

# INTRODUCTION

Determining how production years and locations influenced end-use quality traits assists breeders, agronomists, and growers, in understanding which hard red spring wheat (HRSW; *Triticum aestivum* L.) varieties are least susceptible to quality fluctuations, and therefore, most desirable to end-users. In order to determine which varieties were more consistent in certain locations, analyses on how end-use quality fluctuates in specific locations was conducted.

When genotypes are tested in different environments, it is observed that the rank or performance of the genotype varies depending on the environment, which is called the genotype-by-environment interaction (GE). The need for growing different cultivars in different locations is due to the GE interaction (Yan et al., 2000). GE interaction is one of the major challenges for plant breeders. In Peña (2008), the interaction variance for FPC for 30 genotypes in 17 locations was smaller than the variance for genotype. This can indicate a particular genotype can have the potential to produce a specified end-use quality (Peña et al., 2008). In Khazratkulova et. Al (2015), they found significant GE interactions in 30 genotypes for yield, TKW, TWT, GPC, and Gluten traits. Peña (2008) also described previous studies that showed mixograph and baking parameters had a larger variation for environment than genotype, but their GE interaction variance was smaller than genotype by itself. This would indicate that the environment would play a big role in the outcome of those traits, but since the genotype variance is larger than the GE interaction variance, the rank of the genotypes for these traits would still be the same from different environments. The genotype ranking for these traits differed depending on

the environment which demonstrates a complex effect of environments on said traits. Many traits are quantitatively inherited and require appropriate genetic analysis in order to select and breed for their improvement. Most quantitative traits are controlled by many minor genes where their expression is dependent on the environment. In order to detect GE interaction affects you would normally need to test genotypes in several environments within replicated trails. When a large number of genotypes are tested in several environments, resources may limit data collection, and may lead to non-replicated trials. This can lead to problems when trying to analyze trials in different years and locations. It is difficult to analyze GE interactions in non-replicated trials There are various methods in order to help breeders account for this GE interaction and overcome unbalanced, incomplete, or non-replicated data sets (Wu et al., 2012). Two of the most popular methods include mixed linear models and biplot analysis.

Linear mixed model (LMM) analysis can be used for variance component estimation. There are three common approaches which include maximum likelihood (ML), restricted maximum likelihood (REML), and minimum norm quadratic unbiased estimation (MINQUE). ML and REML require normally distributed data and involve intensive iteration. However, MINQUE does not require normally distributed data nor iteration. This allows for faster computation and application to more forms of data. In Wu (2012), the equations and process for LMM analysis is explained (Wu et al., 2012). Effectiveness of selection for a trait depends on the proportion of phenotypic variance which is attributable to genetic variance, a concept referred to as broad-sense heritability or degree of genetic determination A breeder must quantify the proportion of variation attributed to genotype, environment, and GE interactions, in order to quantify gain from

selection that can be expected and to choose the appropriate selection methods. However, the interactions between genotype and environment can present difficulties in the evaluation of the best genotype. Efficiency of selection for a specific trait in a breeding program depends on its level of heritability where higher values lead to higher selection response. Heritability is determined by the proportion of variance attributed to genotype relative to that of genotype-by-environment interaction and random error variance (Caffé-Treml, 2010). Proportional variance components are extremely useful in determining the proportion of variance due to the variance component for each trait, which is the objective of most GE LMM analysis. LMM analysis results can show how much proportion each effect in the GGE model contributes to the trait.

Biplot analysis for multi-year variety trial data of a year-location-genotype trait four-way table can be converted into various two-way tables. The most common method of conversion is by using a combination of year and location called the environment. Multi-year data analysis has three objectives when it comes to genotype-by-environment analysis, which are mega-environment analysis, test location evaluation, and genotype evaluation. Multi-year analysis can be used to show the repeatability across years of trials and various evaluations. The biggest challenge to multi-year analysis is incomplete and unbalanced data sets, but the problem has been addressed by Yan (2013) with the development of singular value decomposition (SVD) to estimate or predict the missing values. Mega-environment analysis, location and genotype evaluation is then conducted using the completed data set (Yan, 2014). Yan (2015) explains a mega-environment as an area of a crop's growing region that is fairly homogenous and produces similar results. Differentiation happens when genotypes perform differently in subregions across

multiple years. Because of this, genotype evaluation is based on mean performance, and selection based on mean performance may not be the correct method due to genotypes that are best in all mega-environments but may not be the best in any of them. The main purpose of analysis is to optimize a variety evaluations and recommendation for certain areas. Analyzing a mega-environment by creating a GGL + GGE biplot, which is a genotype x genotype-by-location biplot with the genotype x genotype-by-environment (location + year), biplot is the best approach. It allows the visualization of genotype (G) vs. GE, genotype-by-location (GL) vs GE, or genotype-by-year (GY) and genotype-by-location-by-year (GLY) (Yan, 2015). In Yan (2015), explains that mega-environment and location evaluation are given increasingly more attention because they are prerequisites for effective genotype evaluation. Mega-environment and location analysis needs to be based on multiple years because the environments in a single year is only a sample of the environment of a whole (Yan, 2015).

Biplot analysis has limitations similar to other analysis procedures. SVD is a major limitation when it comes to unbalanced data, because SVD requires a complete two-way table. Breeders find it hard to have balanced multi-year data due to the introduction and removal of various experimental cultivars in their data sets. This is because inferior genotypes are usually dropped, and new genotypes are added yearly. Many research objectives require multi-year data, and therefore, unbalanced data or incomplete data becomes a significant limitation in analysis. In Yan (2013), the proposed procedure for the estimation of the missing values in a two way table, where a multiyear data set of year-location-genotype trait dataset is converted into a two-way table where the environment is year-location, is where the missing cells are first filled in with 0 and

then subjected to SVD analysis and the missing values are predicted from the results of the first two principal components (PC).

GGE variance component estimation and biplot analysis is used to predict and estimate how varieties, locations, and years influenced HRSW grown in South Dakota and provide statistical analyses for the trends earlier in this study. The focus is on statistical analysis to identify the best locations and varieties for consistent end-use quality. This information will be helpful for growers, breeders, and millers in identifying the interactions of genotypes and environments to explain stability of varieties and traits in different counties throughout South Dakota.

This study may help breeders in selecting varieties to cross with, and to select environments to test for specific traits. It will enable growers to identify the best varieties for their locations and will show millers and buyers the best locations and varieties to purchase from in the hope to increase value and production of HRS wheat grown in South Dakota. The objective of this experiment was to determine how production years and locations influenced end-use quality traits.

# MATERIALS AND METHODS

One thousand four hundred twenty-three HRSW samples were collected from the seed testing laboratory at South Dakota State University. These samples represented certified seed samples from twelve varieties, seven years and thirty-eight counties throughout South Dakota. Variety, county, and year were the three main factors for consideration, but counties were also further grouped into districts categorized by the USDA to help compare with production results presented in Table 3.1. The USDA crop reporting districts in South Dakota represented in this study are Central, East Central, North Central, North East, North West, South Central, South East, and West Central (Figure 3.1). Six varieties included in this study were developed in South Dakota while remaining six were from North Dakota or Minnesota. Varieties analyzed were 'Advance', 'Barlow', 'Brick', 'Briggs', 'Faller', 'Forefront', 'Howard', 'Prosper', 'RB07', 'Select', 'Steele-ND', and 'Traverse'. Since the evaluated samples were from certified seed samples submitted to the Seed Testing Laboratory, they were a random collection, though dependent on those available for production at that time of submission. The data set was unbalanced and not all varieties were grown in each county or year. All varieties were represented by at least 40 samples with a few having almost 300 samples. Also, the number of samples per county and year were random and unbalanced with certain counties that produce more wheat on average, having more samples represented in the study.

All samples were evaluated for twenty-one quality traits, which were divided into three categories, kernel, flour, and dough quality traits. Three kernel quality parameters

were measured; test weight (TWT), thousand kernel weight (TKW), and grain protein content (GPC). Flour traits measure were flour extraction (EXT), ash content (ASH), flour protein content (FPC), gluten index (GI), wet gluten content (WGC), dry gluten content (DGC), and water-binding (WB). The dough quality traits measured were water absorption (ABS), top-of-envelope variables, peak time (EPT), peak value (EPV), left-of-peak slope (ELS), right-of-peak slope (ERS), mixing stability (MSE), and mid-lines variables peak time (MPT), peak value (MPV), left-of-peak slope (MLS), right-of-peak slope (MRS), mixing stability (MSM). The summary statistics and trends for each factor year, county, and variety, are reported and explored in chapter 2.

## Data Analysis

Data was collected on 21 parameters; three kernel quality traits, seven flour quality traits, and eleven were collected from mixograph analyses. Statistical analysis of each parameter was performed using R. Pearson correlation coefficients were computed on the entire dataset using R Package 'agricolae'. The dataset was not balanced due to missing observations for certain year, county, and variety combinations. Therefore, an extended GGE mixed model for genotype-location-year (GLY) was used for variance component estimation and is shown in the equation below:

$$y_{ijkr} = \mu + G_i + L_j + Y_k + (GL)_{ij} + (GY)_{ik} + (LY)_{jk} + (GLY)_{ijk} + \epsilon_{ijkr}$$

Where $y_{ijk}$ is the observed value for replicate $r = 1\ to\ n_r$ , genotype $i = 1\ to\ n_g$, location $j = 1\ to\ n_l$, and year $k = 1\ to\ n_y$; $\mu$ is the grand mean; $G_i$ is the main effect of genotype $i = 1\ to\ n_g$; $L_j$ is the main effect of location $j = 1\ to\ n_l$; $Y_k$ is the main effect

of year $k = 1\ to\ n_y$; $(GL)_{ij}$ is the interaction effect between genotype $i$ and location $j$ ; $(GY)_{ik}$ is the interaction effect between genotype $i$ and year $k$; $(LY)_{jk}$ is the interaction effect between location $j$ and year $k$; $(GLY)_{ijk}$ is the three-way interaction effect between genotype $i$, location $j$, and year $k$; $\epsilon_{ijk}$ is the random error for replication $r$ genotype $i$ at location $j$ in year $k$. Due to the structure of the data set and the unbalanced randomness of the samples evaluated, this study included three important components; model evaluation, linear mixed model analysis for variance component estimation and heritability, and biplot analysis. Data analysis procedures were performed for model evaluation and variance component estimation as described by (Wu et al., 2012). Biplot analysis for multiyear data was performed using GGE biplot as described by (Yan, 2014).

## Model Evaluation

Genetic model evaluation for three variance component parameter configurations were evaluated. Type I error, testing power, bias, and standard error were calculated for each variance component (Wu et al., 2012) based on 500 simulations using the lmm.jack.simu function in R package ‘minque’, developed by Dr. Jixiang Wu of South Dakota State University (Wu, 2014).

## Variance Component Estimation

Statistical analysis of each parameter was performed as described by (Lu, 2017). by using R (R Core Team, 2018). Variance components were estimated using the lmm.jack function in R Package ‘minque’, with genotypes, counties, and years and their

interactions considered as random effects. Each variance component was reported as the variance component estimation, proportion of total variance, and heritability. Lmm.jack is an R function for linear mixed model analysis with integration two linear mixed model approaches (Restricted maximum likelihood and MINQUE) and a jackknife technique, but in this case MINQUE estimation was used. The objective of LMM analysis is estimating variance components. Proportional variance components can also be calculated by taking the ratio for each variance component by the total variance. The phenotypic variance ($V_p$) was defined as $V_p = V_G + V_{GL} + V_{GY} + V_{GLY} + V_e$ where, $V_G = \sigma_G^2$ for genotypic effects; $V_{GL} = \sigma_{GL}^2$ for GL effects; $V_{GY} = \sigma_{GY}^2$ for GY effects; $V_{GLY} = \sigma_{GLY}^2$ for GLY effects. The ratio of $V_G/V_P$ is considered the heritability of the genotype. The ratio $V_G/(V_{GL} + V_{GY} + V_{GLY})$ can also be useful in comparing the genotype effect to the GE interaction effect (Wu, 2003). Genetic, location, and year effects can also be estimated by adjusted unbiased prediction approach (AUP) which can help determine the individual effects for each genotype, location, and year from the population mean. The predicted effects were also estimated using the R package “minque”.

## Biplot Analysis

Mega-environment analysis is conducted by the generation of a GGE biplot to display the genotype-by-environment with each location represented by multiple points. Then a GGL + GGE biplot is generated with locations defined as a single point based on the mean coordinates of the specific location(Yan, 2015). The GGL+GGE biplots were than overlaid with a “which-won-where” process in which the best performing variety is identified in each mega-environment. First you connect all varieties with a polygon that

are on the lines or contained in it. Then starting from the biplot origin, draw straight lines that are perpendicular to each side of the polygon. These perpendicular lines are equality lines. The line perpendicular to the polygon side connecting certain varieties is the equality line between the varieties, and any environments on that would be equal. The equality lines divide the biplot into mega-environments and the environments fall into one of them. Therefore, each mega-environment will have a vertex of the polygon with a variety on it. That variety will then be the best performing variety in that mega-environment and for any environments falling within that mega-environment. The environment values are the average coordinates of the locations in various years. Locations are analyzed by the distance an environment is from the biplot origin which indicates its consistency in a mega-environment across years. Environments closest to the origin indicate they varied widely in that environment across years (Yan, 2014). Trait biplots for year, county, and variety were also created with a standard deviation scale and double centered analysis.

# RESULTS AND DISCUSSION

## Correlations

Pearson correlation coefficients between all quality traits across all varieties, counties and years is summarized in table 3.2. Only the significant correlations are present in the table. GPC was significantly correlated with all kernel and flour quality traits and only significantly correlated with the dough quality traits EPV, MLS, MPV, MRS, and MSM. GPC had a high positive correlation with WGC, DGC, and WB with coefficient values above 0.70. ABS and FPC have correlation values above 0.96, but that was due to FPC and GPC both measuring protein and ABS was calculated from FPC. TWT was significantly correlated with all kernel and flour traits and ERS, MRS, and MSM. Most of the correlations are small, except for the correlation between TWT and TKW which had a correlation coefficient of 0.48. TKW had a significant correlation between all traits except for WGC, ELS, and MSE, with the highest correlation values being with EPT and MPT and EXT at -0.42, -0.43, and 0.42. ASH was significantly correlated to all kernel and flour quality traits and the dough quality traits EPT, MPT, and MSE, but are all very small values. ABS and FPC was significantly correlated with all quality traits except ERS. ABS and FPC have a correlation coefficient of 1, because ABS was calculated from FPC. EXT was significantly correlated with most kernel and dough quality traits, but not correlated with any gluten parameters. GI was moderately negatively significantly correlated with the other gluten parameters WGC, DGC, and WB with correlation coefficients around 0.50. GI was also moderately correlated with EPT and MPT with correlation coefficients of 0.56 and 0.57. The results revealed that peak

mixing time could be used as an indicator of gluten strength. WGC, DGC, and WB are all significantly correlated with dough quality traits. Dough quality traits were mostly significantly correlated with each other. There are only a few traits highly significantly correlated with others that are not calculated from each other in any way. These traits were GPC and FPC with WGC, DGC, and WB and have coefficients of around 0.80. These correlations confirmed the trends in the summary statistics.

## Model Evaluation

The model evaluation is summarized in table 3.3. The table shows the estimate power, type 1 error, and bias of the model. The first evaluation was conducted with all pre-set values set to zero for all variance components except random error. This pre-set was used to determine Type 1 error for all the variance components. All variance components were set to 20 for the second evaluation, which evaluates the testing powers of each component. The third evaluation had a mix of preset values, where year, county, and variety were set to 0 and the other variance components were set to 20, which tests for type 1 error for the main effects, while testing the power for the remaining interaction and error variance components. Model evaluations were subjected to 500 simulations at a significance level of 0.05. Results show that type 1 error for all variance components was around 7% or less for the first evaluation. The second evaluation showed the testing power for all variance components was very close to 100% with year having the lowest testing power at 94%, which was still very high. The third evaluation where the type 1 error was evaluated for just the main effects showed a slight increase in error by about 10% for all three main effects. Each model evaluation also presents the bias in each estimation. Bias was low for all three models but is somewhat larger in comparison for

the main effects in the mixed set evaluation. These results showed the GLY model had very low type 1 error while having a very high testing power, which revealed that the model used presents unbiased results.

## Variance Component Estimation

The relationship of genetic variance to environmental and error variance provides the most information to breeding programs. If a genotype represents a larger proportion to other variance components, it may be grown and selected for in a larger area and would thus require fewer selection cycles and indicates the ability to use early generation selection. The smaller the genotypic proportion, the less influence a variety had on the trait in question, and suggests a large GE interaction which would require more growing cycles and locations in order to rank a variety on its performance for a certain trait (Caffe-Treml et al., 2010). The variance component estimation is summarized for all 21 traits in tables 3.4 through 3.9. Even though some genotype-environment combinations had no replications, some of the combinations did, which allowed the partition of the genotype-by-environment interactions effects from the error variance. Traits heavily influenced by error variance could be due to both measurement error and genotype-by-environment interaction. Inflated measurement error was likely for some traits (Lu, 2017).

### Kernel Quality Traits

Tables 3.4 and 3.7 contain the variance component and proportional variance component estimation for kernel quality traits. All variance components were significant

at a significance level of 0.05 for GPC and TKW except for the year-variety-county interaction effect. All variance components were significant for TWT, except for county, year-variety, and year-variety-county interaction effects. Random error represented the majority of variation for GPC. Other than random error, the environment (year-county interaction) effect was greatest for GPC, and only slightly being larger than the variation for the variety effect at 12.21% and 11.59% respectively. The heritability for GPC was 15.05%. TKW was mainly influenced by year and represented the majority of variation at 39.39%. The heritability for TKW was 12.95%. Random error represented the largest proportion of variance for TWT. Variety effect represented the next largest variation for TWT at 24.44%. The heritability for TWT was much larger compared to the other traits at 34.97%. According to the results, TKW was influenced the most by year and would require multi-year studies in order to overcome the environment effect and select for it.

**Flour Quality Traits**

Tables 3.5 and 3.8 summarize the variance component and proportional variance component estimation for flour quality traits. All main effects were significant for all of the flour quality traits. Random error represented the highest proportion of variance for all traits. None of the interaction effects were significant for EXT. Year influenced EXT more than the other effects at 25.65%, and the heritability was 10.08%. Year-variety and year-county interaction effects were both significant for ASH. Variety represented the highest proportion of variance at 30.63% and the heritability was 41.06%. All interaction effects were significant for FPC except for year-variety-county interaction effect. Variety also influenced FPC more than any other effect at 13.56% and the heritability was 17.36%. Year-variety and year-county interaction effects were both significant for GI.

Variety represented the highest proportion of variance at 39.61% and the heritability was 44.23% which was the largest for any trait. All interaction effects were significant for WGC except for year-variety-county interaction effect. The environment (year-county interaction) effect was largest for WGC, and year represented the largest main effect at 11.23% and 7.55%, respectively. The heritability for WGC was 7.87%. All interaction effects were significant for DGC except for year-variety-county interaction effect. The environment (year-county interaction) effect was largest for DGC, and year represented the largest main effect at 9.72% and 9.69%, respectively. The heritability for WGC was 8.22%. All interaction effects were significant for WB except for year-variety-county interaction effect. The environment (year-county interaction) effect was largest for WB, and variety represented the largest main effect at 10.77% and 6.93%, respectively. The heritability for WGC was 8.90%. In conclusion, the flour traits ASH and GI had main effect proportional variance closest to random error and the largest heritability overall.

**Dough Quality Traits**

Tables 3.6 and 3.9 summarized the variance component and proportional variance component estimation for dough quality traits. County and year effects were only significant in a few traits and ABS, EPT, EPV, MPT, and MPV were the only parameters with random error less than 60% and represented the highest proportion of variance for all traits. Due to the large random error variance, ABS, EPT, EPV, MPT, and MPV were the only dough quality traits analyzed further. ABS was the only trait with all main effect and most interaction effects being significant with the exception of year-variety-county effects. Variety effect represented the largest proportion of variance for ABS at 13.63% and heritability was 17.43%. Top-of-envelope peak time only had year and variety and

year-county interaction effects as significant. Variety also represented the largest proportion of variance at 22.91% and heritability was 28.08%. Year, variety and year-county and variety-county interaction effects are significant for EPV. Year also represented the largest proportion of variance at 15.58% and heritability was 16.46%. MPT only had year and variety and year-county interaction effects as significant. Variety also represented the largest proportion of variance at 23.86% and heritability was 29.11%. Year, variety and year-county and variety-county interaction effects are significant for MPV. Year also represented the largest proportion of variance at 14.10% and heritability was 10.77%. Overall for dough quality traits ABS and the peak parameters were the best traits explained by the model. For peak parameters, EPT and MPT, variety effect accounted for the most variation for main effects whereas for peak values, EPV and MPV, the year effect accounted for the most variation. The peak time parameters had the largest heritability compared to the other traits. With such high random error variance for most of the mixograph parameters, the model may have the same problem in estimating the dough quality traits as the previous kernel and flour traits.

**Selection and Heritability**

As described by (Caffé-Treml, 2010), the efficiency of selection for a specific trait in a breeding program depends on its level of heritability where higher values lead to higher selection response. For kernel quality traits, according to Lu (2017), GPC had a heritability ranging from 61% to 77%, and TWT had a heritability ranging from 75% to 90% which were much higher than the heritability estimated in this study. For flour quality traits, FPC had a heritability ranging from 63% to 77%, GI had a heritability ranging from 63% to 77%, WGC had a heritability ranging from 43% to 70%, DGC had a

heritability ranging from 26% to 48%, and WB had a heritability ranging from 39% to 61%. These previous results were much higher than the results calculated in this study. This may be due to high random error variance, and traits heavily influenced by error variance could be due to both measurement error or may indicate the model may not fit the unbalanced data set well. Therefore, extrapolation of the results may be limited, even though the model evaluation showed the results were unbiased, have high estimate power and low type 1 error rates. From all the variance component estimation results, it is hard to determine statistically from the main and interaction effects, the objective of how years and locations, affected the different end-use quality traits, other than TKW in which the random error variance does not account for the highest proportion of variance, and was influenced the most by year and would require multi-year studies in order to overcome the environment effect and select for it. There are no traits where county was the largest influence out of the main effects, while TKW, EXT, WGC, DGC, EPV, MPV, and MLS were influenced the most by the year at, 25.65%, 7.55%, 9.69%, 15.58%, 14.10%, and 5.39%, respectively. However, WGC, DGC, and WB were influenced the most by the year-county interaction at, 11.23%, 9.72%, and 10.77%, respectively. Since, the remaining traits were influenced the most by variety effect, and none were influenced the most by county and county-variety interaction, most traits would be considered more consistent from county to county.

## Predicted Effects

Even though variance component estimation may not be able to explain all the variance in the dataset, the adjusted unbiased prediction (AUP) method used to predict

variety, county, and year effects can prove more useful. The predicted effects for all quality traits compared to the population mean are summarized in tables 3.10 through 3.18 and selected traits for variety and county along with the upper and lower limits of the 95% confidence interval for each predicted effect are graphed in figures 3.2 through 3.15.

**Predicted Variety Effect**

Results in the summary statistics were supported by the predicted results from the linear mixed model analysis. Predicted variety effects are graphed in figures 3.2 through 3.8 for selected traits that had lower random error variance in the above variance component estimation. In the figures, the predicted effect, along with the lower and upper limits of a 95% confidence interval for each variety, are the effects compared to the fixed effect population mean. For GPC, most varieties had a significant predicted effect compared to the population mean of 14.33%. Briggs, Barlow, and Steele-ND had the top three highest positive predicted effects. However, the use of confidence intervals allows simultaneous inference for pairwise comparisons. The upper and lower limit values for the 95% confidence interval reveal there was no significant difference between the predicted effects of Briggs, Barlow, and Steele-ND. Traverse, Howard, and Advance had the highest negative predicted effects. However, the predicted effect of Advance was not significant, and therefore was not statistically different than the population mean. Traverse had a larger negative effect and was statistically different than all other varieties. The results for TKW were actually different than the results in the summary statistics. The highest and lowest average results for TKW were Howard and Select,

respectively. However, for predicted effect, Howard and Select were closer to the population mean of 30.20 grams, than most other varieties and Howard does not even have a significant effect and therefore, does not have a statistical difference from the mean. The differing results for variety effect from the summary statistics may be due to the large year influence from the variance component estimation. TWT was similar to GPC where most varieties had a significant effect from 81.46 kg/hl and the predicted effects confirm the results in the summary statistics. Traverse had a very large negative significant effect on TWT. Only a few varieties have a significant effect from 58.91% for EXT, but the highest and lowest significant effects were the same as in the summary statistics, where Howard and Select have the largest positive and negative effects, respectively. Select and Forefront had the largest positive and negative significant effects for ASH content from the average of 0.30%. Flour protein content had similar as GPC with Barlow, Steele-ND, and Briggs having the largest significant effect and Traverse and Advance have the largest negative significant effect from 14.20%. All but one variety had a significant effect for GI. Brick, Advance, and Steele-ND had the top three predicted effects and Brick had the largest significant effect from 90.60. Wet gluten content had the same three largest positive significant effects from 36.09% as FPC and GPC, with Briggs have the largest WGC effect. However, there were no statistical difference between the three varieties. Water absorption effects were similar to FPC, GPC and WGC with the fixed effect mean of 64.90%. For the predicted effects, the peak time traits EPT and MPT, Brick had a very large significant predicted effect compared to the other varieties and Traverse, Briggs, and Prosper had the three largest significant negative effects from 3.50 and 4.30 minutes. Top-of envelope peak value and MPV had very similar predicted

effects with Barlow, Steele-ND, and Faller having the largest positive significant effects and Select, Prosper, and Traverse had the largest negative significant effects from 74.94% and 55.42%. The predicted effect results for varieties confirm the trends in the summary statistics. The results for GPC, FPC, WGC, and ABS revealed that Briggs, Barlow, and Steele-ND had the highest predicted effects. Barlow and Steele-ND also had the highest predicted MPV and EPV values with average MPT and EPT which signifies the best overall end-use quality for varieties. Briggs also had good overall end-use quality traits but had average peak values and the smallest peak time on average. Overall, Traverse had the worst end-use quality. These predicted effects confirmed the results in the summary statistics.

**Predicted County Effects**

The predicted county effects are graphed in figures 3.9 through 3.15 for selected traits that had lower random error variance and larger main effect influence in the variance component estimation. Predicted county effects are one of the more important aspects of determining how production areas influence end-use quality traits. The results for GPC revealed that the counties Faulk, Beadle, and Hutchinson and Brookings, Lyman, and Grant have the three largest positive and negative significant effect from the fixed effect mean, respectively. Thousand kernel weight had the opposite trend in counties as compared to varieties, in which Grant, Deuel, and Hamlin had the largest positive significant effect in TKW, but relatively negative predicted effects for GPC. Test weight had similar results to TKW with the top three largest positive predicted effects with Brown, Sully, and Grant counties, but Sully county actually had a positive

significant effect for GPC. The largest positive significant effects for EXT were from the counties Hughes, Walworth, and Day. Beadle county actually had the largest positive predicted effect but was not significant. Hutchinson, Pennington, and Dewey had the largest negative predicted effects. The results for ASH content revealed that Hutchinson, Hanson, and Beadle had the largest positive significant effects and Grant, Edmunds, and Brookings had the largest negative significant effects for ASH. Flour protein content had similar results as GPC. Faulk, Beadle, and Sully havd the three largest positive significant effects and Brookings, Grant and Edmunds had the three largest negative significant effects for FPC. Gluten index had opposite effects as compared to FPC and GPC, where Roberts, Grant, and Brookings had the largest positive significant effects and Hanson, Beadle, and Campbell had the largest negative significant effects. Wet gluten content and ABS had relatively the same results as FPC and GPC with the same counties having positive and negative effects for each trait. Top-of-envelope peak time and MPT had very similar rankings of counties for predicted effects except that MPT did not have any significant effects for the counties. The three largest positive effects for counties were Dewey, Spink, and Codington and the three largest negative effects for counties were McPherson, Lake, and Beadle. Top-of-envelope peak value and MPV had no significant effects for any counties. The predicted effects had similar results to the summary statistics, except that the top overall counties for end-use quality, which were Faulk Beadle and Hutchinson, were actually in the Central and North Central districts. The worst overall counties for end-use quality were Grant, Brookings, and Edmunds. These results were based on overall significant effects for the traits GPC, FPC, WGC, MPV, and EPV. However, this was different for the trends in the summary statistics. These

results may be due to the fact that overall averages change the rankings for districts. This was supported by the contrasting predicted effects of Edmunds and Faulk counties that have very different results in terms of negative and positive significant effects and were both in the same district. Also, the two major counties represented in the North West district that had the overall best quality results in the summary statistics were Corson and Dewey. They generally had no significant effect either negative or positive from the fixed population mean.

## Biplot Analysis

The problem with variance component estimation in which high random error variance indicates the model may not fit the unbalanced data set well can be overcome using SVD analysis to predict the missing values in biplot analysis using GGE biplot software by Yan (2013). Differentiation happens when genotypes perform differently in subregions across multiple years. Because of this, genotype evaluation is based on mean performance, and selection based on mean performance may not be the correct method due to genotypes that are best in all mega-environments but may not be the best in any of them. The main purpose of mega-environment analysis is to optimize variety evaluations and recommendation for certain areas. Relationships among all variables included in the study can be visualized with Trait biplots for varieties, years, and counties. For each trait, a vector is displayed from the biplot origin to its marker. The cosine of the angle between any two vectors approximates the correlation coefficient between them. Thus, the presence of an acute or obtuse angle between two trait vectors indicates positive or

negative correlations, respectively. A right angle between two vectors indicates that the corresponding traits are uncorrelated (Yan, 2014).

Using mega-environment evaluation and which-won-where methods, location and genotype evaluations were analyzed in biplots in figures 3.16 through 3.26 were created for all 21 kernel, flour, and dough traits. The biplots for GPC, TKW, and TWT explained 48.7%, 36.3%, and 51.7% of the variation, respectively. There were two main mega-environments with Briggs performing the best for the majority of the counties and Select performing the best in the other mega-environment. The larger environment included counties such as Hutchinson, Tripp, Hanson, Hughes, and Kingsbury, and the environment where Select did the best included counties such as Charles and Brookings. There were three main mega-environments for TKW, with Briggs performing the best in the environment with Hyde and Sanborn, Faller performing the best in the environment with Codington and Beadle, and Howard performing the best in the main environment with Hutchinson, Hanson, and Hamlin as the counties with the greatest effect.The results revealed that TWT had two main mega-envrionments: Brick performed the best in the environment with Marshall and Sanborn; Briggs performed the best in the environment with Jerauld and Beadle.

Flour quality mega-environment analysis resulted in very similar biplots for protein and gluten content traits. The biplot for FPC was generally the same as GPC with two mega envrionemtns and the biplot explained 49.8% of the variation. Briggs did better in counties such as Kingsbury, Hutchinson, Hamlin, and Spink and Select did better in Charles Mix, Corson, Campbell and Edmunds. The results for ASH revealed that

almost all counties were in the same mega-environment and performed similarly with Select, having the largest ASH content. Forefront performed the worst in all counties, and the biplot explained 47.7% of the variation. The biplot for EXT explained 44.9% of the variation. Again, there is no apparent effect difference between most of the counties, with them being grouped. The GI plot explained the most amount of variation at 72.6%. However, most of the varieties were near the origin, and the counties were also very similar. Dry gluten content evaluation was very similar to ABS, with Briggs performing the best in most counties, and there were two main mega-environments. The biplot for WB explained 43.8% of the variation. There were two main mega-environments, with Traverse performing the best in the environment with Hutchinson, Hamlin, and McPherson and Briggs performing the best in the main environment with Jerauld and Hyde counties with the greatest effect. There were two main mega-environments for WGC, in which Traverse performed the best in the environment with Hutchinson, Hamlin, and McPherson and Briggs performed the best in the main environment with Jerauld and Hyde counties with the greatest effect. The biplot for WGC explained 41.6% of the variation and had very similar results as WB.

Dough quality traits had similar results to kernel and flour quality traits. In mega-environment analysis for ABS, there were three main environments in which counties within an environment performed similarly. All counties where grouped in 2 of the 3 mega-environments except for Douglas county which is in the same mega-environment as Traverse, and Traverse had the largest negative predicted effect for ABS. Also, Douglas county only had one sample represented in the study, and therefore the true effects cannot be determined. For the majority of most counties, Briggs performed the

best in regards of ABS, while counties such as Charles Mix, Select performed the best. The biplot for ABS explained 50% of the variation. The biplot for MLS explained 47.1% of the variation and there were two main mega-environments. Traverse performed the best in the environment with Beadle, Hutchinson, and Hamlin and Briggs performed the best in the environment with Charles Mix, Hyde, and Minnehaha. The biplot for MPT explained 61.4% of the variation. There was one main mega-environment, with Brick performing the best. The biplot for MPV explained 38.2% of the variation. There were three main mega-environments, with Traverse performing the best in the environment with Hamlin, Brick performing the best in the environment with Faulk and Spink and Briggs performing the best in the main environment with Charles Mix, Dewey and Deuel. The biplot for MRS was not able to use the which-won-where method nor mega-environment analysis because of the lack of pattern identified between counties and varieties. There were three main mega-environments, and the biplot for MSE explained 39% of the variation. Select performed the best in the environment with Kingsbury, Deuel, and Dewey and Barlow performed the best in the main environment with Hutchinson, Hanson, and Hamlin as the counties with the greatest effect. The biplot for MSM explained 46% of the variation with three main mega-environments. Select performed the best in the environment with Marshall and Sanborn, Briggs performed the best in the environment with Charles Mix, Corson, and Jones and Brick performed the best in the main environment with Hutchinson, Hanson, and McPherson as the counties with the greatest effect. Mega-environment analysis for top-of-envelope parameters were similar to mid-line parameter traits and can be referenced in figures 3.16 through 3.26.

Trait biplots are similar to the GGE biplots discussed above, except that the traits are substituted for genotype, location, or year. The data is then scaled with the units removed. Scaling a trait using standard deviation is the most commonly used method in multitrait data analysis. These trait biplots can allow the relations among traits to be understood and to understand the trait profiles of the factor used (Yan, 2014).

Figure 3.27 contains the Location-by-trait biplot (LT), LT biplot allows the analyses of locations for the suitability of producing certain end-use quality. The cosine of the angle between two traits approximates the location correlation between them (Yan, 2014). The biplot reveals the positive relationshups between GPC, FPC, DGC, WGC, WB, MSE and ABS. There are also positive realtionshups between TWT, GI, EPT, MPT, and ERS. Positive relationships between MRS, TKW, and EXT. And finally, MSM, EPV, MLS, ASH, and MPV. The biplot also reveals that most counties are close to the origin showing that they are stable or have similar effect betwen counties, exvept for the outlier counties, Minnehaha and Moody, which are comprised of a single sample each.

The year-by-trait biplot (YT) is illustrated in figure 3.28. A YT allows the approximate of the year correlation between traits (Yan, 2014). As compared to the LT biplot, more traits are positively correlated with each other. The biplot reveals that MLSm MSM, MPV, EPV, WB, WGC, DGC, and MSE are highly positively correlated while GI, MRS, MPT, ERS, EPT, ASH, and ELS are also highly positively correlated. These two groups are on opposite sides of the biplot which concludes they are negatively correlation for years. The YT biplot also illustrate sthe larger effect of years on traits in which the years are not close to the origin with the group with GI having larger values in 2015, while the other group with WGC having larger values in 2010, 2009, and 2008.

Figure 3.29 contains the genotype-by-trait biplot (GT). The GT biplot also shows the genotype correlation between traits which is similar to the LT and YT biplots. However, GT illustrates the trait profiles for each variety (Yan, 2014). The genotypic correlation for EPT, MPT, GI, MRS, TWT, ASH, and ERS are positively correlated. MSM, EXT, TKW, and MLS are also positively correlated. Finally, DGC, WGC, WB, MPV, EPV, MSE, ELS are positively correlated. ABS, GPC, and FPC are positively correlated with some of the traits in the previous grouping of MSE, an ELS. The biplot also reveals the larger differences in varieties as compared to the smaller differences between locations. The biplot comfirms the previous results that Select, Barlow, and Steele-ND have larger GPC, ABS, and FPC effects well having lower EXT, and TKW effects. Brick, Advance, and Forefront have higher EPT, MPT, GI, MRS, TWT, ERS, and ASH effects. The trait biplots, LT, YT, and GT, are summarized across the whole of the other factors. For example. GT is the pattern for all years and counties and thus may not be completely true in a single year or county, this problem is caused by genotype-by-location interactions. This problem is solved by the previous mega-environment analysis.

Biplot analysis revealed that for most traits there were two main mega-environments where most counties effected traits similarly to others in the same mega-environment. Briggs generally performed the best in the major environments for the protein and protein related traits, which support the results from the predicted effects. Brick and Select also performed the best for certain traits and environments. The trait biplots helps conclude that traits are more variable between years and varieties as compared to the LT biplot which reveals that traits are less variable between locations. This is also shown in the previous variance component estimates in which year and

varieties are the largest main effects for traits, but county effect is not the largest proportional effect for any trait. This indicates that specific county effects are not large enough to ignore the importance of selecting the proper variety and testing it in multiple years.

# CONCLUSION

To explain the trends between traits in the summary statistics, correlations between all traits were conducted that revealed there were only a few traits highly significantly correlated with other traits that were not calculated from each other in any way. These traits were GPC and FPC with WGC, DGC, and WB and have coefficients of around 0.80. The correlations confirm the trends in the summary statistics and may be able to help with either selection or indirect selection in the future. In order to determine which varieties were more consistent in certain locations, evaluations were done to show how end-use quality fluctuated in specific locations and determine how production years and locations influenced end-use quality traits.

This study required statistical analysis on unbalanced, multi-year data, which is a significant limitation in analysis. The various methods to help account for GE interaction and overcome this limitation were mixed linear models and biplot analysis. The model evaluation showed the GLY linear mixed model had very low type 1 error while having a very high testing power, which revealed the model presented unbiased results.

From all the variance component estimation results, it was difficult to determine statistically from the main and interaction effects, the objective of how years and locations, affected the different end-use quality traits. This limitation may be due to high random error variance. Traits heavily influenced by error variance could be due to both measurement error and may indicate the model may not fit the unbalanced data set well and extrapolation of results may be limited, even though the results were unbiased. TKW was the only trait in which the random error variance does not account for the highest

proportion of variance and was influenced the most by year. Focusing on the main effects, there were no traits where county represented the largest influence out of the main effects, while TKW, EXT, WGC, DGC, EPV, MPV, and MLS were influenced the most by the year at, 25.65%, 7.55%, 9.69%, 15.58%, 14.10%, and 5.39%, respectively. However, WGC, DGC, and WB were influenced the most by the year-county interaction at, 11.23%, 9.72%, and 10.77%, respectively. Since, the remaining traits were influenced the most by variety effect, and none were influenced the most by county and county-variety interaction, most traits would be considered more consistent from county to county. However, these results were much lower than what is reported in previous studies and limits the validity of the variance component estimation.

The predicted effect results for varieties confirm the trends in the summary statistics. For GPC, FPC, WGC, and ABS, Briggs, Barlow, and Steele-ND had the highest predicted effects. Barlow and Steele-ND also have the highest predicted MPV and EPV values with average MPT and EPT which signifies the best overall end-use quality varieties. Briggs also had good overall end-use quality traits but had average peak values and the smallest peak time. Overall, Traverse had the worst end-use quality. The predicted effects for counties had similar results to the summary statistics, except that the top overall counties for end-use quality, which were Faulk Beadle and Hutchinson, were actually in the Central and North Central districts. The worst overall counties for end-use quality were Grant, Brookings, and Edmunds. These results were based on overall significant effects for the traits GPC, FPC, WGC, MPV, and EPV. However, this is somewhat different for the trends concluded in the summary statistics. This may be due to the fact that overall averages change the rankings for districts. This is supported by the

contrasting predicted effects of Edmunds and Faulk counties that have very different results in terms of negative and positive significant effects. Also, the two major counties represented in the North West district that had the overall best quality results in the summary statistics were Corson and Dewey. They generally had no significant effect either negative or positive from the fixed population mean.

The problem with variance component estimation, in which high random error variance indicates the model may not fit the unbalanced data set well, may be overcome using SVD analysis to predict the missing values in biplot analysis using GGE biplot software. For most traits there were two main mega-environments where the counties effect traits similarly to others in the same mega-environment. Briggs generally performed he best in the major environments for the protein and protein related traits, which support the results from the predicted effects. Brick and Select also performed the best for certain traits and environments. However, since there were only two main mega-environments, biplot analysis failed to differentiate between the effects for most counties, according to the biplot, they performed very similar in regard to most traits.

These results confirm the correlation between gluten content traits and protein content traits. However, the unbalanced dataset limited the determination of specific GE influences for most traits from variance component estimation. In order to properly determine how production year and locations influenced end-use quality traits, more samples and a more controlled experiment of design may be needed to validate results and reduce the random error to make more explicit conclusions. With the help of predicted estimates from AUP and biplot analysis this study was able to reveal higher

quality producing varieties and counties in South Dakota. The results determined Briggs, Steele-ND, and Barlow resulted in higher end-use quality wheat for most counties in South Dakota. This study also revealed the higher end-use quality effect for counties in the North Central and North West districts.

The overall results with the combination of biplots and variance component estimation is that traits are more variable between years and varieties as compared to the counties. The biplot results reveal that traits are less variable between locations. This is confirmed by variance component estimates in which year and varieties are the largest main effects for traits, but county effect is not the largest proportional effect for any trait. This indicates that specific county effects are not large enough to ignore the importance of selecting the proper variety and testing it in multiple years.

According to the U.S Hard Red Spring wheat regional quality report produced by US Wheat Associates in 2017 (U.S. Wheat Associates, 2017), South Dakota had average end-use quality and protein in comparison to the northern and western HRSW producing areas. However, this study showed that the locations vary in the end-use quality of wheat produced. Therefore, when end-users acquire wheat from a certain elevator, it may result in lower quality wheat. Since elevators acquire grain from their local area, it may be detrimental to them and reduce their ability to supply end-users with higher quality wheat. For instance, the higher wheat producing areas in South Dakota may be a major source of grain sourced by end-users and have lower end-use quality. If these elevators or end-users source grain from different parts of South Dakota, primarily the North Central and North West districts, they may be able to acquire higher end-use quality wheat and in

the same step increase demand of HRSW in the lower producing but higher quality counties of South Dakota.

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Table 3.1. USDA Crop Reporting Districts, Spring Wheat Production in South Dakota

| Ag District | ACRES HARVESTED | ACRES PLANTED | PRODUCTION, BU | YIELD, BU / ACRE |
|---|---|---|---|---|
| CENTRAL | 188,500 | 237,500 | 6,972,000 | 37 |
| EAST CENTRAL | 11,100 | 11,200 | 576,000 | 51.9 |
| NORTH CENTRAL | 319,000 | 326,500 | 14,336,000 | 44.9 |
| NORTHEAST | 119,000 | 122,000 | 6,326,000 | 53.2 |
| NORTHWEST | 185,000 | 199,000 | 7,023,000 | 38 |
| OTHER DISTRICTS[a] | 85,900 | 92,400 | 3,146,000 | 36.6 |
| SOUTH CENTRAL | 48,900 | 53,000 | 1,890,000 | 38.7 |
| SOUTHWEST | 7,600 | 8,400 | 261,000 | 34.3 |
| SOUTH DAKOTA[b] | 965,000 | 1,050,000 | 40,530,000 | 42 |

[a]OTHER DISTRICTS: Combination of West Central and South East

[b]Total production for entire state of South Dakota

Table 3.2. Pearson Correlation Coefficients[a] between all Quality Traits.

| | GPC[b] | TWT | TKW | ASH | ABS | FPC | EXT | GI | WGC | DGC | WB | ELS | EPT | EPV | ERS | MLS | MPT | MPV | MRS | MSE | MSM |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GPC | | | | | | | | | | | | | | | | | | | | | |
| TWT | -0.22** | | | | | | | | | | | | | | | | | | | | |
| TKW | -0.35** | 0.48** | | | | | | | | | | | | | | | | | | | |
| ASH | 0.28** | -0.31** | -0.35** | | | | | | | | | | | | | | | | | | |
| ABS | 0.96** | -0.15** | -0.26** | 0.28** | | | | | | | | | | | | | | | | | |
| FPC | 0.96** | -0.15** | -0.26** | 0.28** | 1.00** | | | | | | | | | | | | | | | | |
| EXT | -0.26** | 0.08** | 0.42** | -0.37** | -0.17** | -0.17** | | | | | | | | | | | | | | | |
| GI | -0.17** | 0.26** | -0.22** | -0.13** | -0.18** | -0.18** | | | | | | | | | | | | | | | |
| WGC | 0.78** | -0.19** | | 0.20** | 0.82** | 0.82** | | -0.58** | | | | | | | | | | | | | |
| DGC | 0.79** | -0.15** | -0.06* | 0.17** | 0.83** | 0.83** | | -0.38** | 0.93** | | | | | | | | | | | | |
| WB | 0.73** | -0.19** | 0.06* | 0.21** | 0.76** | 0.76** | | -0.65** | 0.98** | 0.83** | | | | | | | | | | | |
| ELS | | 0.06* | | 0.09** | 0.06* | 0.06* | | | 0.06* | 0.08** | 0.05* | | | | | | | | | | |
| EPT | | | -0.42** | 0.09** | -0.06* | -0.06* | -0.26** | 0.56** | -0.38** | -0.25** | -0.43** | | | | | | | | | | |
| EPV | 0.35** | | 0.13** | | 0.44** | 0.44** | 0.11** | | 0.41** | 0.46** | 0.36** | 0.15** | -0.18** | | | | | | | | |
| ERS | | 0.10** | -0.06* | | | | -0.10** | 0.16** | -0.09** | -0.08** | -0.09** | | 0.10** | -0.24** | | | | | | | |
| MLS | 0.20** | | 0.22** | | 0.26** | 0.26** | 0.14** | -0.35** | 0.39** | 0.34** | 0.39** | | -0.42** | 0.38** | -0.20** | | | | | | |
| MPT | | | -0.43** | 0.09** | -0.10** | -0.10** | -0.28** | 0.57** | -0.42** | -0.28** | -0.46** | | 0.91** | -0.25** | 0.18** | -0.60** | | | | | |
| MPV | 0.39** | | 0.17** | | 0.48** | 0.48** | 0.10** | -0.21** | 0.52** | 0.53** | 0.49** | 0.12** | -0.31** | 0.81** | | 0.48** | -0.38** | | | | |
| MRS | -0.16** | 0.15** | -0.19** | | -0.19** | -0.19** | -0.12** | 0.53** | -0.44** | -0.36** | -0.46** | | 0.54** | -0.16** | 0.18** | -0.35** | 0.51** | -0.40** | | | |
| MSE | | | | 0.08** | 0.06* | 0.06* | | | 0.08** | 0.09** | 0.07** | 0.97** | -0.06* | 0.20** | -0.26** | 0.08** | -0.06* | 0.11** | -0.06* | | |
| MSM | 0.21** | -0.09** | 0.24** | | 0.28** | 0.28** | 0.16** | -0.48** | 0.48** | 0.41** | 0.48** | | -0.54** | 0.36** | -0.23** | 0.94** | -0.68** | 0.53** | -0.65** | 0.09** | |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight; EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding; ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 3.3. Estimated Type I, testing power, and bias for estimating variance components from 500 iterations of simulated data for the year, variety, and county combinations analyzed.

| Variance Component | Pre-set Value | Type I Error | | | |
|---|---|---|---|---|---|
| | | Estimate | Bias | SE | Power |
| Year | 0 | 0.1087 | -0.1087 | 0.0079 | 0.0180 |
| County | 0 | 0.1720 | -0.1720 | 0.0116 | 0.0520 |
| Variety | 0 | 0.1283 | -0.1283 | 0.0082 | 0.0400 |
| Year:County | 0 | 0.2584 | -0.2584 | 0.0155 | 0.0560 |
| Year:Variety | 0 | 0.2259 | -0.2259 | 0.0143 | 0.0480 |
| County:Variety | 0 | 0.2984 | -0.2984 | 0.0170 | 0.0740 |
| Year:County:Variety | 0 | 0.4402 | -0.4402 | 0.0248 | 0.0680 |
| Residual Error | 20 | 19.9328 | 0.0672 | 0.0411 | 1.0000 |
| Variance Component | Pre-set Value | | | | |
| | | Estimate | Bias | SE | Power |
| Year | 20 | 19.9273 | 0.0727 | 0.6071 | 0.9400 |
| County | 20 | 19.6559 | 0.3441 | 0.3548 | 0.9940 |
| Variety | 20 | 20.1251 | -0.1251 | 0.5089 | 0.9760 |
| Year:County | 20 | 20.1635 | -0.1635 | 0.2077 | 1.0000 |
| Year:Variety | 20 | 20.5430 | -0.5430 | 0.2559 | 1.0000 |
| County:Variety | 20 | 19.7823 | 0.2177 | 0.1787 | 1.0000 |
| Year:County:Variety | 20 | 19.7387 | 0.2613 | 0.1268 | 1.0000 |
| Residual Error | 20 | 20.0375 | -0.0375 | 0.0428 | 1.0000 |
| Variance Component | Pre-set Value | Mixed Set Error | | | |
| | | Estimate | Bias | SE | Power |
| Year | 0 | 1.1938 | -1.1938 | 0.0927 | 0.1540 |
| County | 0 | 1.3495 | -1.3495 | 0.0902 | 0.1620 |
| Variety | 0 | 1.3085 | -1.3085 | 0.0968 | 0.1800 |
| Year:County | 20 | 19.9376 | 0.0624 | 0.2065 | 1.0000 |
| Year:Variety | 20 | 19.7610 | 0.2390 | 0.2741 | 1.0000 |
| Year:Variety | 20 | 20.0272 | -0.0272 | 0.1925 | 1.0000 |
| Year:County:Variety | 20 | 20.1384 | -0.1384 | 0.1441 | 1.0000 |
| Residual Error | 20 | 20.0178 | -0.0178 | 0.0430 | 1.0000 |

Table 3.4. Estimated variance components[a] for kernel quality traits measured on 1423 flour samples collected from 12 varieties grown in 38 counties over 7 years .

| Variance Component | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| V(Year) | 0.1322** | 8.7119** | 1.2864** |
| V(Variety) | 0.1971** | 1.2830** | 2.5673** |
| V(County) | 0.0512* | 1.5210** | 0.4361 |
| V(Year:Variety) | 0.0658** | 1.1571** | 0.0000 |
| V(Year:County) | 0.2074** | 1.9773** | 1.4425** |
| V(Variety:County) | 0.1629** | 0.4318* | 0.5889** |
| V(Year:Variety:County) | 0.0243 | 0.6277 | 0.0679 |
| V(e) | 0.8593** | 6.4010** | 4.1164** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

Table 3.5. Estimated variance components[a] for flour quality traits measured on 1423 flour samples collected from 12 varieties grown in 38 counties over 7 years .

| Variance Component | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| V(Year) | 2.4136** | 0.000136** | 0.0971** | 2.5366** | 1.4391** | 0.2392** | 0.5139** |
| V(Variety) | 0.6445** | 0.000513** | 0.2278** | 38.3042** | 1.1325** | 0.1535** | 0.6019** |
| V(County) | 0.4448* | 0.00025** | 0.0840** | 3.7309** | 1.0518** | 0.1149** | 0.4743* |
| V(Year:Variety) | 0.0845 | 0.000084* | 0.0759* | 2.3054* | 0.5685* | 0.0659 | 0.2684 |
| V(Year:County) | 0.1546 | 0.00004** | 0.1869** | 3.8277** | 2.1357** | 0.2395** | 0.9353** |
| V(Variety:County) | 0.0229 | 0.000035 | 0.1666** | 2.526 | 1.6602** | 0.1656* | 0.7571** |
| V(Year:Variety:County) | 0.5192 | 0.000048 | 0.0145 | 1.1517 | 0.0000 | 0.0000 | 0.0000 |
| V(e) | 5.1223** | 0.00057** | 0.8267** | 42.2945** | 11.0267** | 1.4864** | 5.1300** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

Table 3.6. Estimated variance components[a] for dough quality traits measured on 1423 flour samples collected from 12 varieties grown in 38 counties over 7 years .

| Variance Component | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| V(Year) | 0.2170** | 0.1655** | 4.6596** | 0.0214 | 0.0673 | 0.0000 | 0.1660** | 2.6959** | 0.5716** | 0.1514** | 1.4270** |
| V(Variety) | 0.5134** | 0.2728** | 3.8236** | 5.8894* | 0.4437* | 3.9209 | 0.2759** | 1.6372** | 0.2461** | 0.2813** | 0.7028** |
| V(County) | 0.1844** | 0.0250* | 0.1314 | 2.5619 | 0.0000 | 2.2419 | 0.0049 | 0.1210 | 0.0094 | 0.1454** | 0.2903 |
| V(Year:Variety) | 0.1759** | 0.0133 | 0.4193 | 0.2114 | 0.0776 | 0.1613 | 0.0337 | 0.4543 | 0.0000 | 0.0378 | 0.0439 |
| V(Year:County) | 0.4198** | 0.0287 | 1.8955** | 0.0000 | 0.0000 | 0.0000 | 0.0374** | 1.1342** | 0.7736** | 0.0896 | 1.0017* |
| V(Variety:County) | 0.3741** | 0.0310 | 1.8872** | 10.4401* | 0.5980* | 10.3477 | 0.0008 | 0.8159** | 0.0163 | 0.0624 | 0.1072 |
| V(Year:Variety:County) | 0.0175 | 0.0000 | 0.5348 | 2.1224 | 0.0823 | 1.5308 | 0.0014 | 0.6787 | 0.0253 | 0.0000 | 0.0351 |
| V(e) | 1.8625** | 0.6548** | 16.5251** | 144.0260** | 9.4622** | 154.5008** | 0.6358** | 11.5673** | 8.9520** | 1.4380** | 11.488** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 3.7. Estimated variance components[a] expressed as proportions to the phenotypic variance for kernel quality traits measured on 1423 flour samples collected from 12 varieties grown in 38 counties over 7 years .

| Variance Component | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| V(Year)/VP (%) | 7.77** | 39.39** | 12.24** |
| V(Variety)/VP (%) | 11.59** | 5.80** | 24.44** |
| V(County)/VP (%) | 3.01* | 6.88** | 4.15* |
| V(Year:Variety)/VP (%) | 3.87** | 5.24** | 0.00 |
| V(Year:County)/VP (%) | 12.21** | 8.95** | 13.73** |
| V(Variety:County)/VP (%) | 9.58** | 1.95* | 5.60** |
| V(Year:Variety:County)/VP (%) | 1.41 | 2.84 | 0.64 |
| V(e)/VP | 50.55** | 28.96** | 39.19** |
| Heritability (%) | 15.05 | 12.95 | 34.97 |

[a]*, ** Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight.

Table 3.8. Estimated variance components[a] expressed as proportions to the phenotypic variance for flour quality traits measured on 1423 flour samples collected from 12 varieties grown in 38 counties over 7 years .

| Variance Component | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| V(Year)/VP (%) | 25.65** | 8.13** | 5.77** | 2.63** | 7.55** | 9.69** | 5.93** |
| V(Variety)/VP (%) | 6.85** | 30.63** | 13.56** | 39.61** | 5.96** | 6.24** | 6.93** |
| V(County)/VP (%) | 4.72* | 14.90** | 5.01** | 3.86** | 5.53** | 4.65** | 5.45* |
| V(Year:Variety)/VP (%) | 0.90 | 4.98* | 4.52* | 2.38* | 2.99* | 2.66* | 3.09 |
| V(Year:County)/VP (%) | 1.64 | 2.38** | 11.13** | 3.96** | 11.23** | 9.72** | 10.77** |
| V(Variety:County)/VP (%) | 0.25 | 2.08 | 9.91** | 2.61 | 8.74** | 6.71** | 8.72** |
| V(Year:Variety:County)/VP (%) | 5.51 | 2.87 | 0.87 | 1.20 | 0.00 | 0.00 | 0.00 |
| V(e)/VP (%) | 54.48** | 34.03** | 49.23** | 43.76** | 58.01** | 60.32** | 59.11** |
| Heritability (%) | 10.08 | 41.06 | 17.36 | 44.23 | 7.87 | 8.22 | 8.90 |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding.

Table 3.9. Estimated variance components[a] expressed as proportions to the phenotypic variance for dough quality traits measured on 1423 flour samples collected from 12 varieties grown in 38 counties over 7 years .

| Variance Component | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| V(Year)/VP | 5.76** | 13.89** | 15.58** | 0.01 | 0.62 | 0.00 | 14.36** | 14.10** | 5.39** | 6.86** | 9.45** |
| V(Variety)/VP | 13.63** | 22.91** | 12.78** | 3.55* | 4.14* | 2.26 | 23.86** | 8.54** | 2.32* | 12.75** | 4.66** |
| V(County)/VP | 4.90** | 2.11 | 0.44 | 1.55 | 0.00 | 1.29 | 0.42 | 0.62 | 0.09 | 6.55** | 1.92 |
| V(Year:Variety)/VP | 4.67** | 1.12 | 1.40 | 0.13 | 0.72 | 0.09 | 2.92 | 2.39 | 0.00 | 1.71 | 0.29 |
| V(Year:County)/VP | 11.13** | 2.41* | 6.34** | 0.00 | 0.00 | 0.00 | 3.24** | 5.94** | 7.30** | 4.03 | 6.61** |
| V(Variety:County)/VP | 9.94** | 2.58 | 6.32** | 6.30* | 5.55** | 5.96* | 0.07 | 4.27** | 0.15 | 2.82 | 0.71 |
| V(Year:Variety:County)/VP | 0.46 | 0.00 | 1.78 | 1.27 | 0.79 | 0.89 | 0.13 | 3.54* | 0.24 | 0.00 | 0.24 |
| V(e)/VP | 49.52** | 54.99** | 55.35** | 87.18** | 88.19** | 89.51** | 55.00** | 60.60** | 84.51** | 65.28** | 76.11** |
| Heritability (%) | 17.43 | 28.08 | 16.46 | 3.60 | 4.17 | 2.29 | 29.11 | 10.77 | 2.66 | 15.45 | 5.68 |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

Table 3.10. Variety predicted effect[a] for kernel quality traits.

| Variety | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| ADVANCE | -0.2771 | -0.5464 | 0.7355** |
| BARLOW | 0.466** | 0.1045 | 1.5823** |
| BRICK | 0.1313* | -0.803** | 1.9126** |
| BRIGGS | 0.5118** | -0.0094 | -0.4007* |
| FALLER | -0.2302* | 2.0398** | -0.4324** |
| FOREFRONT | -0.0202 | -0.129 | 0.5988** |
| HOWARD | -0.3358* | 0.6391 | 0.1846 |
| PROSPER | 0.1355 | 1.0924** | -1.0202** |
| RB07 | 0.2429** | -2.2799** | -0.8844** |
| SELECT | 0.1253 | -0.4232* | 0.9056** |
| STEELE-ND | 0.3377** | 1.0402** | 0.9533** |
| TRAVERSE | -1.0872** | -0.7252 | -4.1352** |
| Average | 14.3271** | 30.2022** | 81.4601** |

[a]*, ** Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight; Average: fixed effect mean.

Table 3.11. Variety predicted effect[a] for flour quality traits.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| ADVANCE | -0.3187 | 0.0156** | -0.3691** | 4.18** | -1.7178** | -0.48** | -1.7178** |
| BARLOW | -0.4096** | -0.0047** | 0.5723** | 1.6422** | 1.2738** | 0.6228** | 1.2738** |
| BRICK | -0.1333 | -0.0127** | 0.0138 | 7.4132** | -1.0516** | -0.0108 | -1.0516** |
| BRIGGS | 0.0112 | -0.0132** | 0.4841** | -8.5998** | 1.8046** | 0.4105** | 1.8046** |
| FALLER | 0.8529** | 0.023** | -0.0926 | 2.6012** | -0.3128 | -0.1483 | -0.3128 |
| FOREFRONT | 0.7469** | -0.0372** | -0.1065 | 2.5052** | -0.6412** | -0.3046** | -0.6412** |
| HOWARD | 0.9274** | -0.0145** | -0.2502** | 1.2728 | -0.4732 | -0.3178** | -0.4732 |
| PROSPER | -0.3948 | 0.0274** | 0.133 | -1.6388 | 0.7799** | 0.1936 | 0.7799** |
| RB07 | 0.7191** | -0.0253** | 0.1219** | 2.0213** | 0.2243 | 0.3166** | 0.2243 |
| SELECT | -1.9052** | 0.0382** | 0.0922 | 1.017** | -0.0873 | -0.0121 | -0.0873 |
| STEELE-ND | 0.2472 | -0.0022 | 0.5597** | 3.0453** | 1.0252** | 0.3512** | 1.0252** |
| TRAVERSE | -0.3432 | 0.0055** | -1.1587** | -15.4597** | -0.8239 | -0.6212** | -0.8239 |
| Average | 58.9136** | 0.3002** | 14.2016** | 90.6036** | 36.0857** | 12.8193** | 36.0857** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding; Average: fixed effect mean.

Table 3.12. Variety predicted effect[a] for dough quality traits.

| Variety | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ADVANCE | -0.5493* | 0.4434** | -0.6576* | -2.6806** | 0.0095 | -2.3648** | 0.3739** | -0.6306** | 0.0331 | -0.0625 | 0.0486 |
| BARLOW | 0.8599** | -0.0335 | 3.1724** | 2.4864** | 0.2189 | 1.9856* | -0.0200 | 2.0819** | -0.2753** | 0.1092 | -0.4336** |
| BRICK | 0.0172 | 1.2967** | 0.5641* | -1.4041 | 0.1882 | -1.4348** | 1.2831** | -0.4869** | -0.6892** | 0.7384** | -1.4000** |
| BRIGGS | 0.7309** | -0.8082** | -0.3806 | -1.4798* | 0.6987** | -1.8694 | -0.8103** | 0.7871* | 0.5747* | -0.5238** | 1.0725** |
| FALLER | -0.1395 | -0.0002 | 1.4124** | 2.6753 | 0.5254** | 1.9219** | -0.1614** | 0.8210** | 0.4839** | 0.5384** | 0.0559 |
| FOREFRONT | -0.1665 | 0.0220 | -0.4013 | -1.1566* | -0.3788* | -0.7148 | 0.0068 | -0.5084* | 0.5557 | -0.0352 | 0.6090* |
| HOWARD | -0.3764 | -0.1453* | 0.0655 | -0.2205 | 0.7403 | -0.8476 | -0.2086 | 0.3067 | 0.1727 | 0.4975** | -0.2663 |
| PROSPER | 0.1999* | -0.2982** | -1.6341** | 0.1028 | -0.7228 | 0.7657 | -0.3444** | -1.3590** | 0.1258 | -0.1477 | 0.3112 |
| RB07 | 0.1803* | 0.0401 | -0.2582 | -0.9167 | -0.3728 | -0.4856 | 0.1727 | -0.0232 | 0.0536 | -0.4354** | 0.4327* |
| SELECT | 0.1360 | 0.0764 | -0.6610* | 2.2290* | 0.5617 | 1.4566* | 0.3048** | -0.2030 | -0.9527** | 0.1519** | -1.1503** |
| STEELE-ND | 0.8384** | -0.0217 | 2.8800** | 3.9437* | -0.0530 | 3.5053* | -0.1129* | 1.6943** | -0.2756 | 0.3241** | -0.6061** |
| TRAVERSE | -1.7308** | -0.5715** | -4.1017** | -3.5790* | -1.4153** | -1.9179 | -0.4836** | -2.4799** | 0.1933 | -1.1548** | 1.3264** |
| Average | 64.9022** | 3.5007** | 74.9407** | 23.9620** | -11.5143** | 35.3535** | 4.3047** | 55.4216** | 5.6888** | -1.9242** | 7.6759** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability; Average: fixed effect mean.

Table 3.13. Year predicted effect[a] for kernel quality traits.

| Variety | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| 2008 | 0.1095 | 1.0939** | -0.1846 |
| 2009 | -0.2232** | 2.4205** | 0.5353** |
| 2010 | -0.1032 | 3.5413** | 0.8623** |
| 2011 | 0.4595** | -4.7101** | -2.111** |
| 2012 | 0.3531** | -2.621** | -0.7545** |
| 2013 | 0.0112 | -1.1707** | 0.5303* |
| 2015 | -0.607** | 1.4461** | 1.1222** |
| Average | 14.3271** | 30.2022** | 81.4601** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight; Average: fixed effect mean.

Table 3.14. Year predicted effect[a] for flour quality traits.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| 2008 | 1.2995** | -0.0135** | 0.1249 | 1.3965 | 0.5343 | 0.3541* | 0.5343 |
| 2009 | 1.5614** | -0.0063** | -0.102 | -0.9835** | 0.5938** | 0.2028** | 0.5938** |
| 2010 | 1.5358** | 0.0036 | 0.0394 | -2.8094** | 1.3779** | 0.4659** | 1.3779** |
| 2011 | -2.052** | 0.0054** | 0.2685** | -0.5412 | 0.3366** | 0.0919 | 0.3366** |
| 2012 | -1.3104** | 0.0092** | 0.2772** | 0.4148 | 0.1573 | 0.1511 | 0.1573 |
| 2013 | -1.3622** | 0.016** | 0.018 | 1.1895* | -0.6995** | -0.3267* | -0.6995** |
| 2015 | 0.3279 | -0.0143** | -0.6261** | 1.3333* | -2.3003** | -0.939** | -2.3003** |
| Average | 58.9136** | 0.3002** | 14.2016** | 90.6036** | 36.0857** | 12.8193** | 36.0857** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding; Average: fixed effect mean.

Table 3.15. Year predicted effect[a] for dough quality traits.

| Variety | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2008 | 0.1900 | 0.0243 | -0.0304 | -0.0876 | -0.2601 | 0.0000 | 0.0405 | -0.1335 | -0.2751 | 0.0388 | -0.3102 |
| 2009 | -0.1515 | -0.4602** | 1.6868** | 0.0498 | 0.0638 | 0.0000 | -0.4644** | 1.3037** | 0.4440* | -0.2341** | 0.7352** |
| 2010 | 0.0608 | -0.5334** | 3.1798** | -0.0136 | -0.1849 | 0.0000 | -0.6046** | 2.7677** | 1.4809** | -0.7556** | 2.3536** |
| 2011 | 0.4004** | 0.0635 | 0.0267 | 0.0180 | -0.0427 | 0.0000 | 0.0853 | -0.3320 | -0.1379 | 0.0657 | -0.2717 |
| 2012 | 0.4110** | 0.4591** | 0.4672* | 0.0392 | -0.0624 | 0.0000 | 0.3540** | -0.1225 | -0.3778** | 0.2762** | -0.6503** |
| 2013 | 0.0264 | 0.5171** | -2.7076** | -0.0209 | 0.3607 | 0.0000 | 0.5120** | -1.4576** | -0.7551** | 0.2584** | -1.0499** |
| 2015 | -0.9370** | -0.0704 | -2.6226** | 0.0150 | 0.1258 | 0.0000 | 0.0773 | -2.0259** | -0.3790* | 0.3506** | -0.8067** |
| Average | 64.9022** | 3.5007** | 74.9407** | 23.9620** | -11.5143** | 35.3535** | 4.3047** | 55.4216** | 5.6888** | -1.9242** | 7.6759** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability; Average: fixed effect mean.

Table 3.16. County predicted effect[a] for kernel quality traits.

| Variety | GPC[b] (12% moisture basis | TKW (grams) | TWT (kg/hl) |
|---|---|---|---|
| Beadle | 0.4021** | -1.1684** | -0.7802 |
| Brookings | -0.4589** | 1.5651** | 0.4241** |
| Brown | -0.0391 | 0.9172** | 1.05** |
| Campbell | 0.06 | 0.802* | 0.8286** |
| Charles Mix | 0.2583** | -1.043** | 0.0303 |
| Clark | -0.0864 | 0.1219 | 0.4104** |
| Codington | 0.0145 | 0.5871 | 0.0585 |
| Corson | 0.1356 | -0.9652** | 0.0584 |
| Day | -0.2643** | 1.4604** | 0.7797** |
| Deuel | -0.1139 | 2.0925** | 0.3904 |
| Dewey | 0.0338 | -1.0049 | -0.3465 |
| Douglas | -0.1152 | 0.5085 | -0.019 |
| Edmunds | -0.2683** | -0.1745 | 0.2856* |
| Faulk | 0.4179** | -0.2093 | -0.5017 |
| Grant | -0.3109** | 3.2625** | 0.8885** |
| Hamlin | -0.1164 | 1.9233** | 0.7229** |
| Hand | 0.1824** | -0.5465** | -0.2665** |
| Hanson | 0.0958 | -1.6266 | -1.0778 |
| Hughes | 0.2502 | -1.0805** | 0.0304 |
| Hutchinson | 0.3317* | -1.6256** | -1.4717* |
| Hyde | -0.0973** | -0.127 | -0.0467 |
| Jerauld | -0.2037** | -0.6025 | -1.0378** |
| Jones | -0.1569* | -1.5228** | -0.3627* |
| Kingsbury | -0.1626 | -0.9212 | -0.6025 |
| Lake | 0.0417 | 1.2498** | 0.0025 |
| Lyman | -0.4329* | -0.7866** | 0.2623 |
| Marshall | 0.1611* | 1.7156** | 0.6884** |
| McPherson | 0.1948** | -0.6158 | -0.2073 |
| Minnehaha | -0.1536 | -0.4325 | 0.3356 |
| Moody | 0.3244 | -0.1032 | -0.2726 |
| Pennington | 0.0498 | 1.0696 | 0.5733 |
| Potter | 0.1407 | -0.2281 | -0.1765 |
| Roberts | -0.152 | 0.8617* | 0.5147 |
| Sanborn | 0.0036 | 0.2983 | -0.4506 |
| Spink | -0.1009 | -1.3617** | -0.8555** |
| Sully | 0.2014* | -0.6449* | 0.9454** |
| Tripp | 0.1253 | -2.0585** | -1.0883** |
| Walworth | -0.1918* | 0.4136* | 0.2842 |
| Average | 14.3271** | 30.2022** | 81.4601** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]GPC: grain protein content; TKW: Thousand Kernel weight; TWT: test weight; Average: fixed effect mean.

Table 3.17. County predicted effect[a] for flour quality traits.

| Variety | EXT[b] (%) | ASH (14% moisture basis) | FPC (14% moisture basis) | GI | WGC (%) | DGC (%) | WB (%) |
|---|---|---|---|---|---|---|---|
| Beadle | 1.497 | 0.0238** | 0.4451** | -3.3448* | 1.6897** | 0.5805** | 1.6897** |
| Brookings | 0.6619** | -0.0219** | -0.5444** | 2.9821** | -1.7605** | -0.5271** | -1.7605** |
| Brown | -0.0444 | 0.0026 | -0.001 | 0.8879 | -0.2005 | -0.0686 | -0.2005 |
| Campbell | -0.6876* | -0.0011 | 0.0649 | -3.8946** | 1.0184** | 0.1188 | 1.0184** |
| Charles Mix | -0.2091 | 0.0158* | 0.3472** | -1.3615 | 0.906** | 0.2265* | 0.906** |
| Clark | 0.0606 | -0.0074* | -0.1042 | 1.638 | -0.7554 | -0.2686* | -0.7554 |
| Codington | -0.6416 | -0.0166** | -0.0138 | 0.3807 | -0.4424 | -0.1108 | -0.4424 |
| Corson | -0.0341 | -0.0004 | 0.1385 | -1.9047* | 0.9203* | 0.3185* | 0.9203* |
| Day | 0.7276** | -0.019** | -0.349** | 2.0303** | -1.2279** | -0.3779** | -1.2279** |
| Deuel | 0.1507 | -0.0198** | -0.1306* | -1.1636 | -0.0507 | -0.021 | -0.0507 |
| Dewey | -1.805** | 0.0226** | 0.0676 | 1.7812* | -0.2505 | -0.0025 | -0.2505 |
| Douglas | 0.2463 | -0.0125 | -0.1872 | 2.0615 | -0.9008 | -0.2464 | -0.9008 |
| Edmunds | 0.6054** | -0.0244** | -0.3862** | -1.4657** | -0.5212* | -0.3065** | -0.5212* |
| Faulk | -0.2245 | 0.0165** | 0.5573** | -1.5829** | 2.0951** | 0.7098** | 2.0951** |
| Grant | 0.3792 | -0.0358** | -0.4673** | 3.3055** | -1.8299** | -0.6018** | -1.8299** |
| Hamlin | 0.0469 | 0.0057 | -0.0697 | -0.7224** | 0.2722 | -0.0328 | 0.2722 |
| Hand | 0.0324 | 0.001 | 0.1139** | -0.8297 | 0.2879 | 0.0958 | 0.2879 |
| Hanson | -0.137 | 0.0255** | 0.0556 | -2.1686** | -0.0693 | -0.0829 | -0.0693 |
| Hughes | 0.9837** | 0.0156** | 0.4235 | -0.9135 | 1.203 | 0.4145 | 1.203 |
| Hutchinson | -0.9077* | 0.0287** | 0.3498** | -1.3138 | 0.5839 | 0.2592* | 0.5839 |
| Hyde | -0.334 | 0.0056 | -0.0916 | -0.026 | -0.1444 | -0.1269 | -0.1444 |
| Jerauld | -0.395 | 0.0076 | -0.3806** | 1.607* | -1.2278** | -0.3759* | -1.2278** |
| Jones | -0.3909** | 0.0155** | -0.0477 | -0.464 | -0.174 | -0.0693 | -0.174 |
| Kingsbury | 0.6952** | 0.001 | -0.2455 | 0.7556 | -1.1333** | -0.3886** | -1.1333** |
| Lake | -0.1749 | -0.0032 | 0.021 | -1.5015* | 0.4609 | 0.123 | 0.4609 |
| Lyman | -0.5784* | 0.0109** | -0.5094 | 2.3993** | -1.6664** | -0.6227* | -1.6664** |
| Marshall | 0.3498 | -0.0172** | 0.1795* | -0.5932** | 0.413* | 0.138* | 0.413* |
| McPherson | 0.316 | 0.0008 | 0.2592** | -0.4661 | 1.2373** | 0.5257** | 1.2373** |
| Minnehaha | 0.0018 | 0.0007 | -0.2129 | 0.7386 | -0.5763 | -0.1714 | -0.5763 |
| Moody | -0.356 | -0.0064 | 0.3762 | -0.3845 | 1.2405 | 0.4047 | 1.2405 |
| Pennington | -1.5058** | 0.0034 | 0.1418 | -2.6606 | 0.9554 | 0.2118 | 0.9554 |
| Potter | 0.2046 | -0.0094** | 0.2288* | 1.4886* | 0.5898* | 0.1888* | 0.5898* |
| Roberts | 0.4944* | -0.0208** | -0.2456** | 3.6709** | -1.3422** | -0.3167** | -1.3422** |
| Sanborn | -0.1663 | 0.0064 | -0.0252 | -1.5869 | 0.3241 | 0.0823 | 0.3241 |
| Spink | 0.423* | 0.0006 | -0.1088 | 1.2641** | -0.8804** | -0.1955* | -0.8804** |
| Sully | 0.2504 | 0.0075** | 0.3538** | 0.5113 | 1.0317** | 0.484** | 1.0317** |
| Tripp | -0.2804 | 0.017** | 0.1795* | -1.5275** | 0.5897 | 0.1798 | 0.5897 |
| Walworth | 0.7462** | -0.0189** | -0.1824* | 2.3734** | -0.6652** | -0.148** | -0.6652** |
| Average | 58.9136** | 0.3002** | 14.2016** | 90.6036** | 36.0857** | 12.8193** | 36.0857** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]EXT: flour extraction; ASH: ash content; FPC: flour protein content; GI: gluten index; WGC: wet gluten content; DGC: dry gluten content; WB: water-binding; Average: fixed effect mean.

Table 3.18. County predicted effect[a] for dough quality traits.

| County | ABS[b] (%) | EPT (minutes) | EPV (%) | ELS (%) | ERS (%) | MSE (%) | MPT (minutes) | MPV (%) | MLS (%) | MRS (%) | MSM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Beadle | 0.6516** | -0.3436** | -0.4591 | -2.0742 | 0 | -0.6494 | -0.0772 | -0.3318 | -0.0312 | -0.3961 | 0.3127 |
| Brookings | -0.8065** | 0.1304 | 0.0539 | -0.2072 | 0 | -0.1734 | 0.0576 | 0.0139 | 0.0249 | 0.136 | 0.0939 |
| Brown | -0.0044 | 0.1215* | 0.0953 | 0.3328 | 0 | -0.6167 | 0.0259 | 0.0973 | 0.0341 | -0.1243 | 0.3096 |
| Campbell | 0.0894 | -0.2143 | -0.4552 | -1.675 | 0 | -0.8766 | -0.0463 | -0.1376 | -0.0112 | -0.5985** | 0.2553 |
| Charles Mix | 0.5004** | -0.1168 | 0.2559 | 4.2281 | 0 | 5.2373 | -0.007 | 0.1465 | -0.0473 | -0.2082* | -0.3680 |
| Clark | -0.1449 | 0.1159 | -0.2476 | 0.3801 | 0 | 0.4962 | 0.0983 | -0.1511 | -0.0434 | 0.1642 | -0.4992 |
| Codington | -0.0242 | 0.2495** | 0.0489 | 0.3066 | 0 | 0.9418 | 0.0653 | 0.1744 | -0.0017 | 0.3923 | -0.1078 |
| Corson | 0.2055 | 0.1635** | 0.0608 | -0.2615 | 0 | -0.8328 | 0.0463 | -0.122 | -0.0765 | -0.1595* | -0.5896 |
| Day | -0.5105** | 0.1584* | 0.0435 | -1.0667 | 0 | -1.4227 | 0.0631 | -0.0559 | -0.0346 | 0.1717** | -0.3644 |
| Deuel | -0.1959 | -0.0671 | 0.1701 | -2.9847 | 0 | -2.7136 | -0.0339 | 0.0544 | 0.0185 | 0.0817 | 0.1165 |
| Dewey | 0.1257 | 0.3294** | 0.3461 | 1.434 | 0 | 1.4857 | 0.1292 | 0.3471 | -0.0391 | 0.3630** | -0.4281 |
| Douglas | -0.2705 | 0.0971 | -0.3306 | -1.3485 | 0 | -1.4822 | 0.0148 | -0.3686 | -0.0597 | 0.0377 | -0.5219 |
| Edmunds | -0.5600** | 0.0144 | -0.3646 | 0.1147 | 0 | 0.2498 | -0.0159 | -0.2405 | 0.0004 | 0.4037** | -0.2828 |
| Faulk | 0.8238** | 0.004 | 0.4405 | -0.5045 | 0 | -0.4519 | 0.0111 | 0.4513 | 0.0649 | -0.4965** | 0.9120 |
| Grant | -0.6943** | 0.0181 | -0.0278 | 1.0767 | 0 | 0.7170 | -0.0052 | -0.1137 | -0.0024 | 0.0507 | -0.0932 |
| Hamlin | -0.1158 | -0.0526 | 0.0537 | 0.695 | 0 | 0.7167 | -0.0208 | -0.3984 | -0.0359 | 0.3303** | -0.5412 |
| Hand | 0.1746* | -0.0183 | 0.0196 | -0.3235 | 0 | -0.8034 | -0.0308 | 0.022 | 0.0092 | 0.1194* | -0.0039 |
| Hanson | 0.0789 | -0.1600* | -0.0417 | -1.7894 | 0 | -0.5509 | -0.0442 | -0.1739 | 0.0155 | -0.0019 | 0.1208 |
| Hughes | 0.6357 | -0.1386 | 0.129 | -0.9411 | 0 | -1.8982 | -0.1091 | 0.4171 | 0.1097 | -1.1754** | 1.6679 |
| Hutchinson | 0.5208* | -0.1353 | 0.2747 | -0.8765 | 0 | -1.8817 | -0.0149 | 0.325 | 0.0874 | -0.3869** | 0.6350 |
| Hyde | -0.1372 | 0.0165 | -0.0803 | -1.6977 | 0 | -2.1617 | -0.0127 | 0.0341 | -0.0035 | 0.0499 | -0.0954 |
| Jerauld | -0.5602** | -0.1235 | -0.1754 | 0.0998 | 0 | -0.2903 | 0.0106 | -0.3779 | -0.1109 | 0.3740** | -1.1554 |
| Jones | -0.0638 | 0.045 | -0.0558 | 0.1405 | 0 | -0.0412 | -0.0002 | 0.0076 | 0.028 | 0.079 | 0.2108 |
| Kingsbury | -0.3892 | 0.0855 | -0.2135 | 1.843 | 0 | 2.6979 | 0.0134 | -0.2549 | 0.0285 | 0.3338 | -0.0274 |
| Lake | 0.0271 | -0.2648** | -0.1629 | 1.6865 | 0 | 2.9468 | -0.0795 | -0.0682 | 0.0285 | -0.3688 | 0.6130 |
| Lyman | -0.7412 | -0.1448 | -0.6679 | 0.572 | 0 | 0.5429 | 0.0571 | -0.2332 | -0.0319 | 0.0509 | -0.4268 |
| Marshall | 0.2621** | -0.0941 | 0.0401 | -0.6728 | 0 | -1.3738 | -0.0576 | 0.0904 | 0.0365 | 0.0793 | 0.2245 |
| McPherson | 0.3852* | -0.1997** | 0.456 | 1.692 | 0 | 2.0045 | -0.0605 | 0.5475 | 0.0343 | -0.3408** | 0.4587 |
| Minnehaha | -0.3136 | 0.0402 | 0.2303 | -0.4064 | 0 | -1.0838 | -0.0612 | -0.0984 | 0.0114 | 0.9819 | -0.3476 |
| Moody | 0.5586 | 0.0717 | 0.048 | 0.2243 | 0 | 0.1561 | 0.0433 | 0.0827 | 0.0075 | -0.1415 | 0.1336 |
| Pennington | 0.2116 | -0.0247 | 0.1464 | 3.6549 | 0 | 6.5799 | -0.0706 | 0.276 | 0.0078 | -0.1964 | 0.2803 |
| Potter | 0.3375* | 0.1327 | 0.2965 | 0.485 | 0 | -0.1252 | 0.0158 | 0.3598 | 0.0251 | -0.1512 | 0.3419 |
| Roberts | -0.3725* | 0.0762 | 0.0407 | 0.5221 | 0 | -0.1825 | 0.0539 | -0.1214 | 0.0001 | 0.2627** | -0.1857 |
| Sanborn | -0.0321 | -0.0759 | -0.0069 | 0.2105 | 0 | -0.2248 | -0.0369 | -0.1202 | -0.0185 | -0.0737 | -0.1189 |
| Spink | -0.1669* | 0.2549** | -0.3083 | -1.4008 | 0 | -1.3501 | 0.089 | -0.2138 | -0.0211 | 0.2346* | -0.4014 |
| Sully | 0.5205** | 0.026 | 0.3362 | -0.616 | 0 | -1.8174 | -0.0334 | 0.1369 | 0.0045 | -0.0996 | 0.1669 |
| Tripp | 0.2667 | -0.1638* | -0.1046 | -0.5705 | 0 | -0.9082 | -0.0232 | 0.1044 | 0.0029 | -0.2046 | 0.0360 |
| Walworth | -0.272** | 0.1869** | 0.1157 | -0.2815 | 0 | -0.8600 | 0.0466 | -0.107 | -0.0108 | 0.4269** | -0.3306 |
| Average | 64.9022** | 3.5007** | 74.9407** | 23.9620** | -11.5143** | 35.3535** | 4.3047** | 55.4216** | 5.6888** | -1.9242** | 7.6759** |

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.

[b]ABS: water absorption; EPT: top-of-envelope peak time; EPV: top-of-envelope peak value; ELS: top-of-envelope left-of-peak slope; ERS: top-of-envelope right-of-peak slope; MSE: top-of-envelope mixing stability; MPT: mid-line peak time; MPV: mid-line peak value; MLS: mid-line left-of-peak slope; MRS: mid-line right-of-peak slope; MSM: mid-line mixing stability.

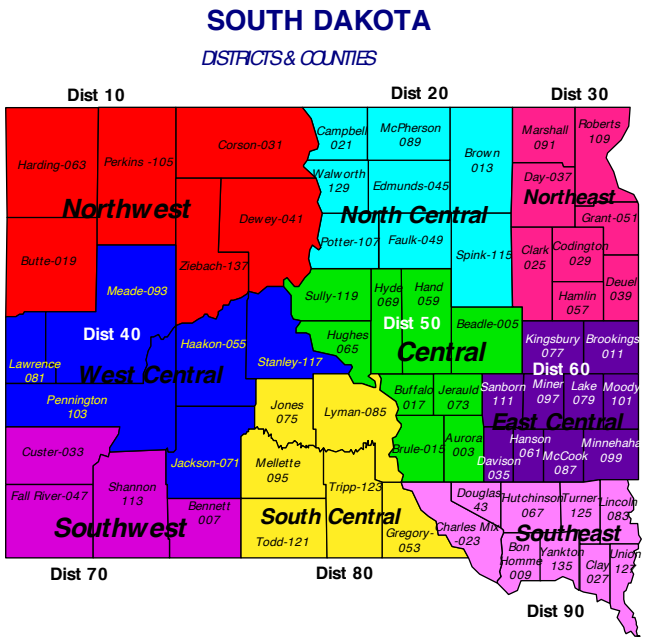



Figure 3.1. USDA, South Dakota Crop Reporting Districts

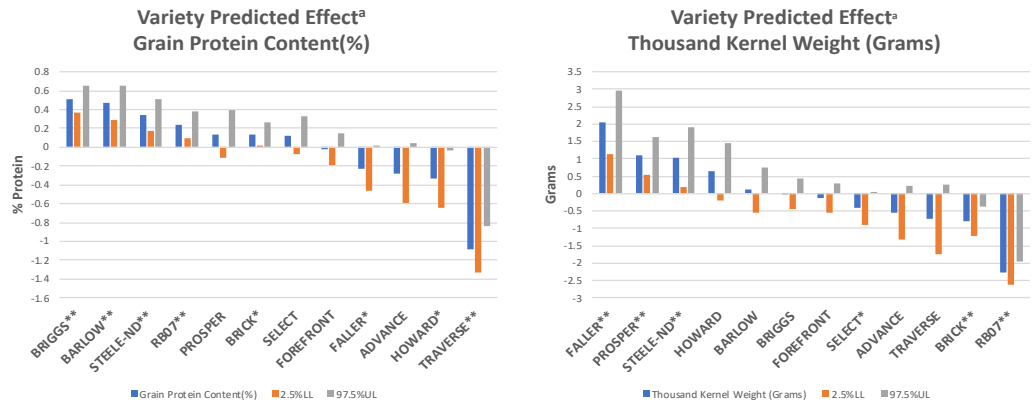



*Figure 3.2. Variety predicted effect for grain protein content and thousand kernel weight, respectively, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

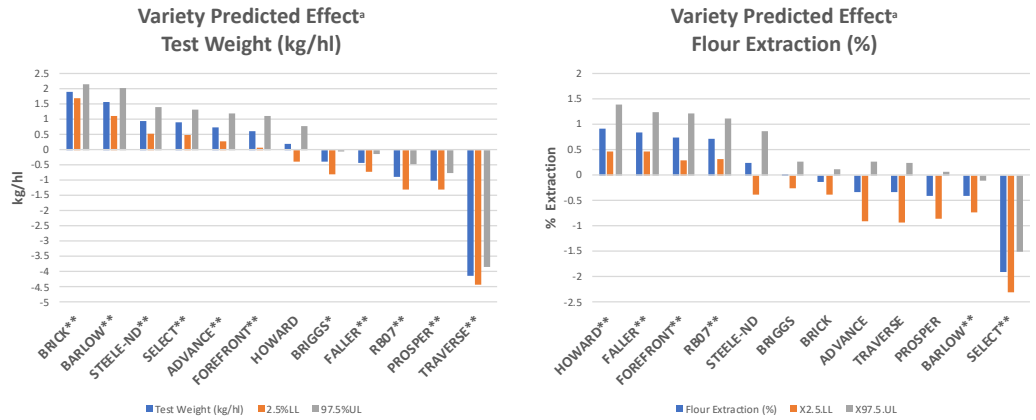



*Figure 3.3. Variety predicted effect for test weight and flour extraction, respectively, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

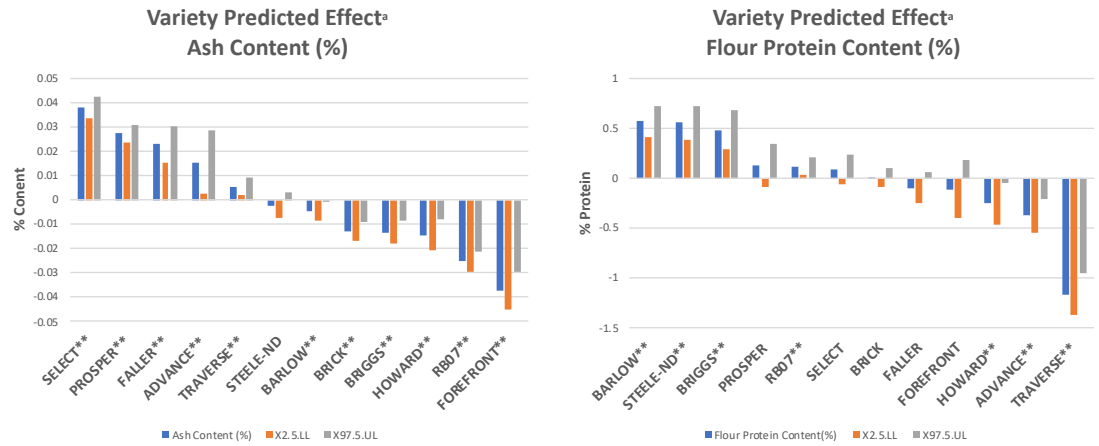



*Figure 3.4. Variety predicted effect for ash content and flour protein content, respectively, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

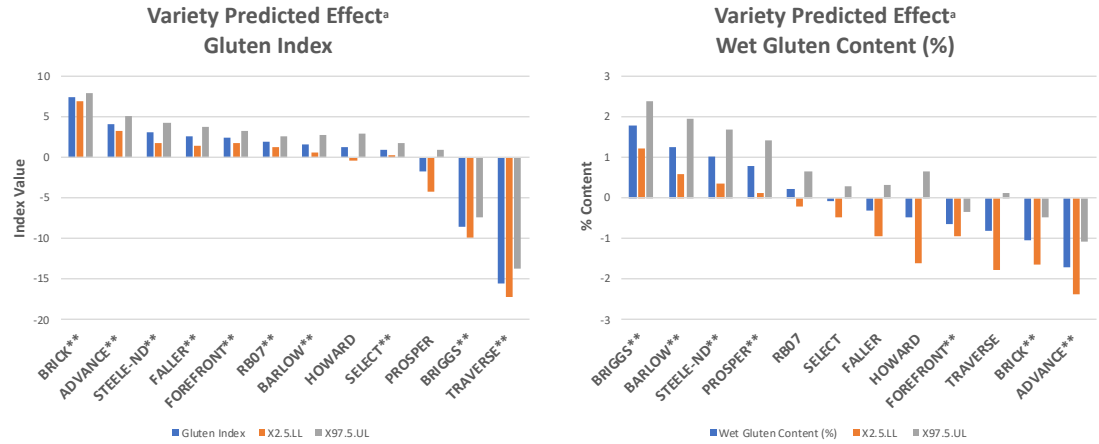



*Figure 3.5. Variety predicted effect for gluten index and wet gluten content, respectively, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

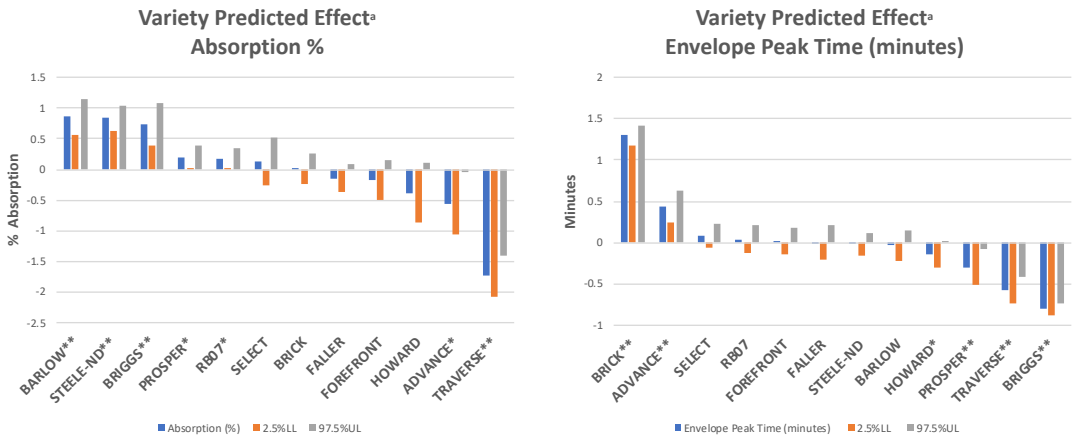



*Figure 3.6. Variety predicted effect for absorption and envelope peak time, respectively, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

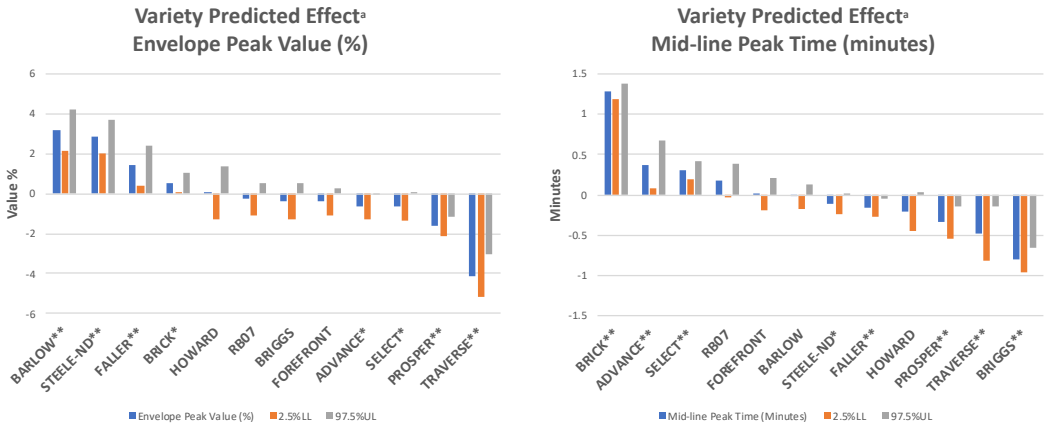



*Figure 3.7. Variety predicted effect for envelope peak value and mid-line peak time, respectively, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

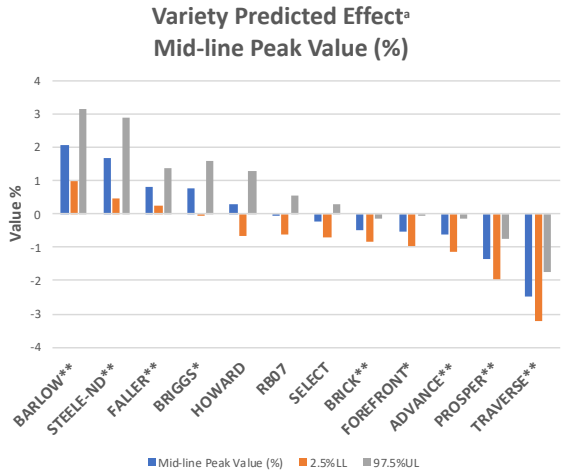



*Figure 3.8. Variety predicted effect for mid-line peak value, using AUP over analysis years and production environments.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

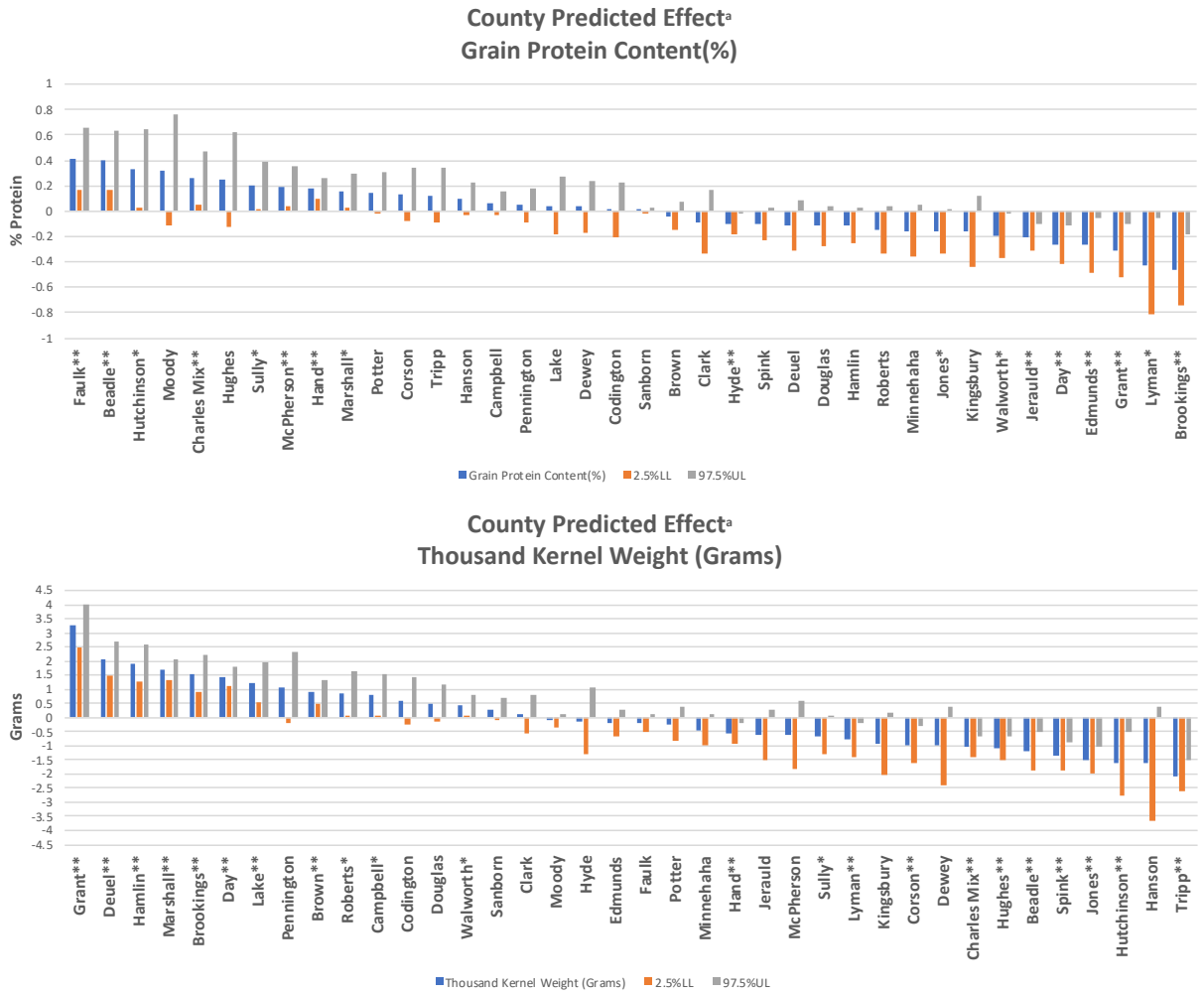



*Figure 3.9. County predicted effect for grain protein content and thousand kernel weight, respectively, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

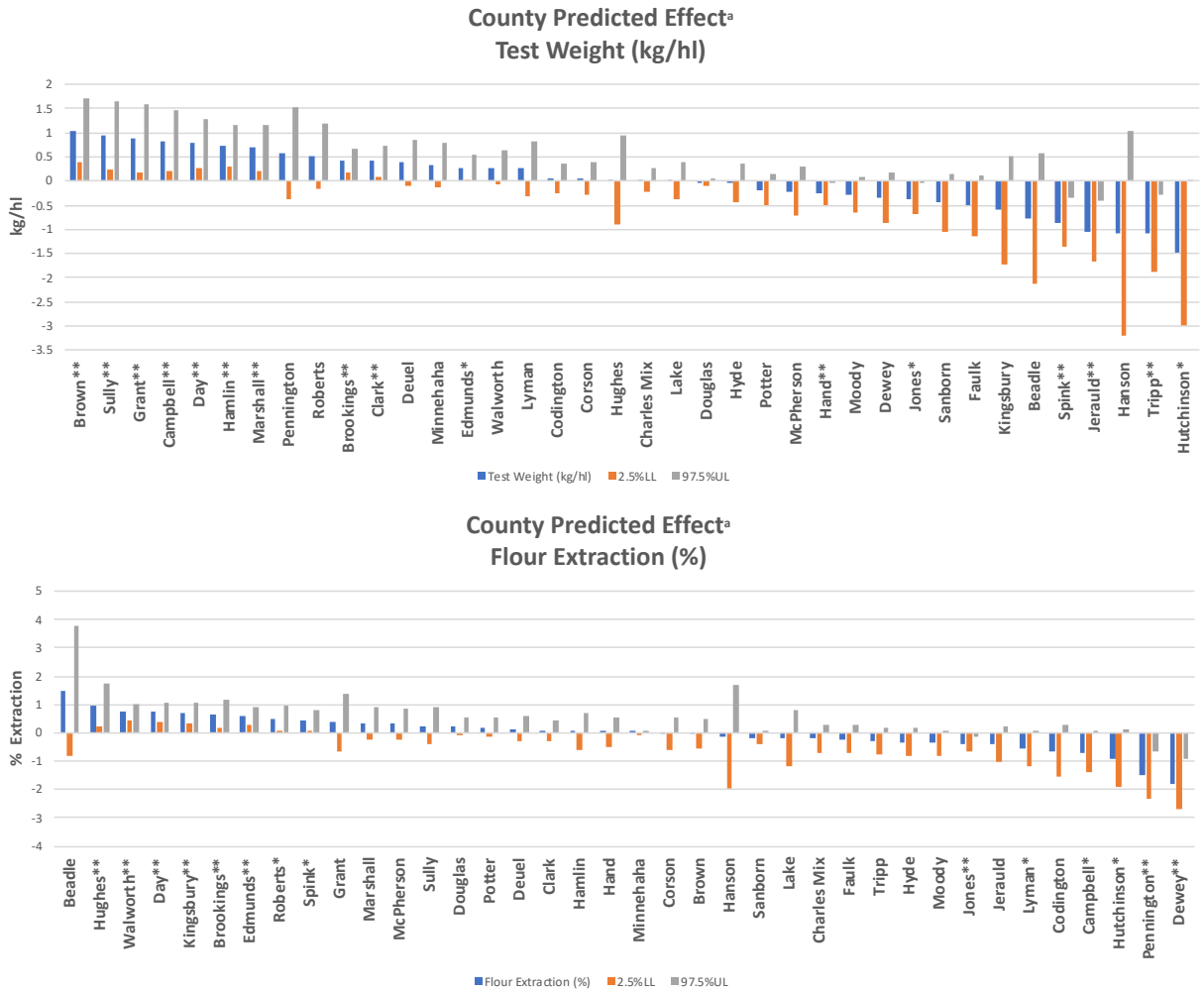



*Figure 3.10. County predicted effect for test weight and flour extraction, respectively, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

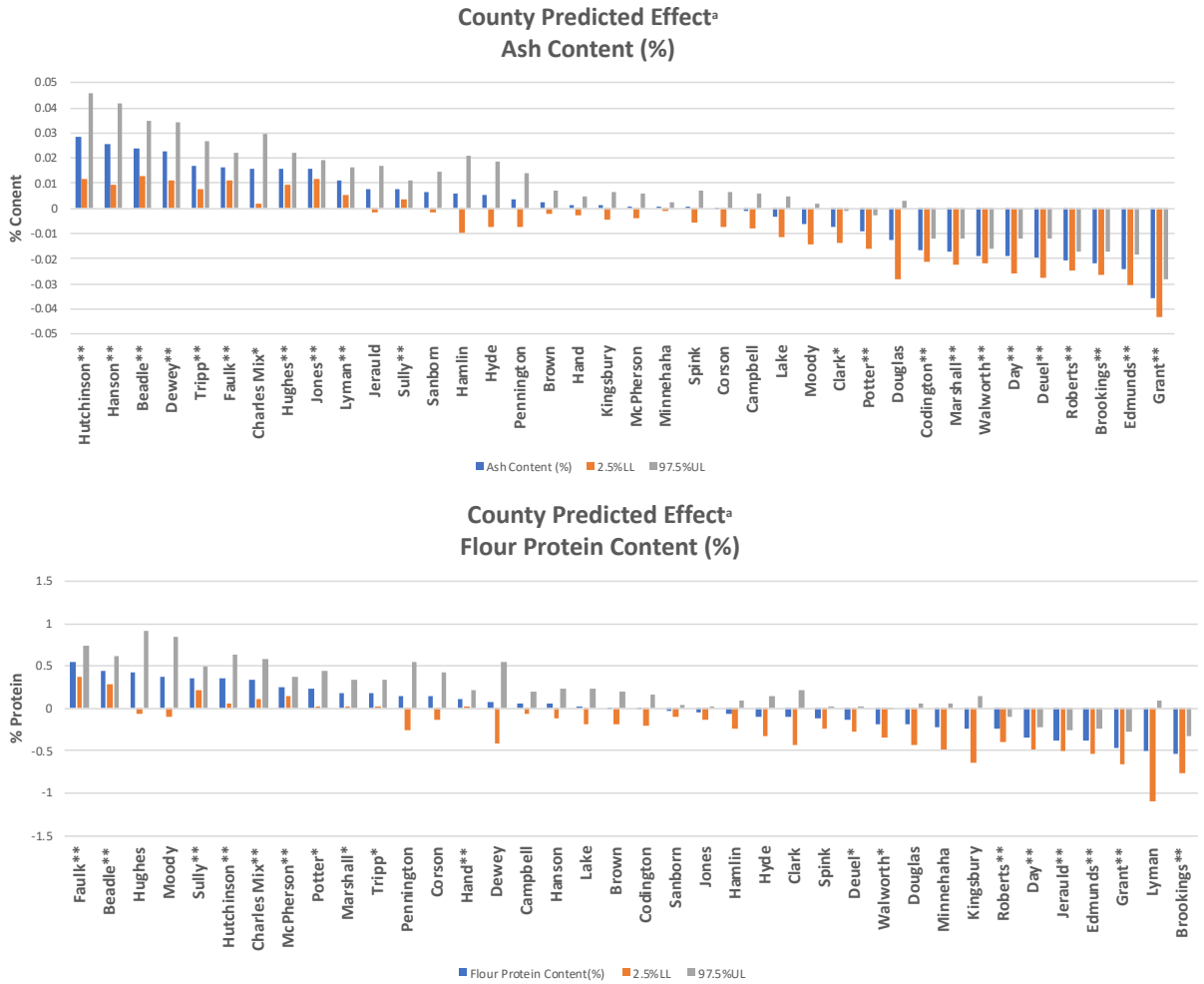



*Figure 3.11. County predicted effect for ash content and flour protein content, respectively, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

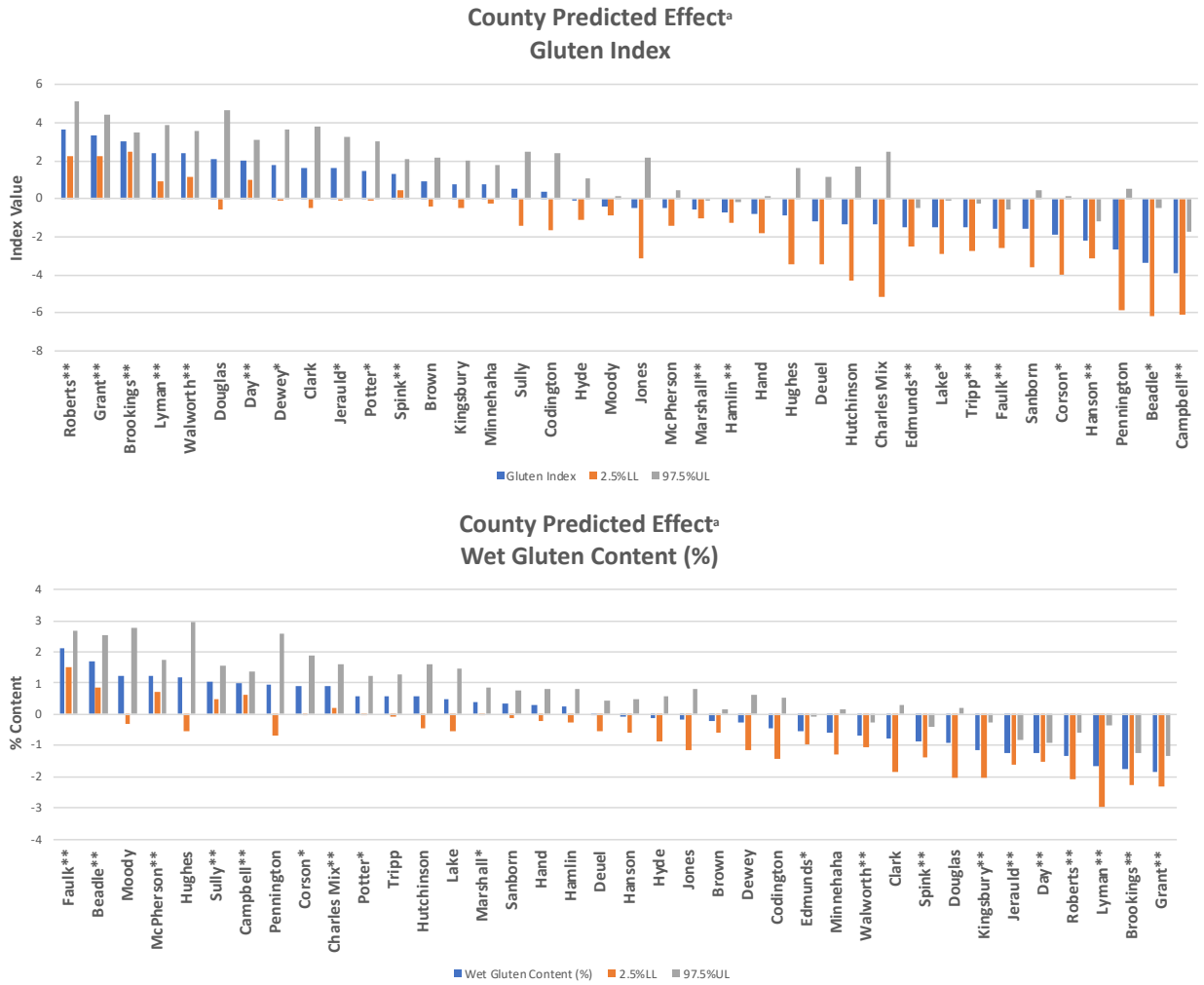



*Figure 3.12. County predicted effect for gluten index and wet gluten content, respectively, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

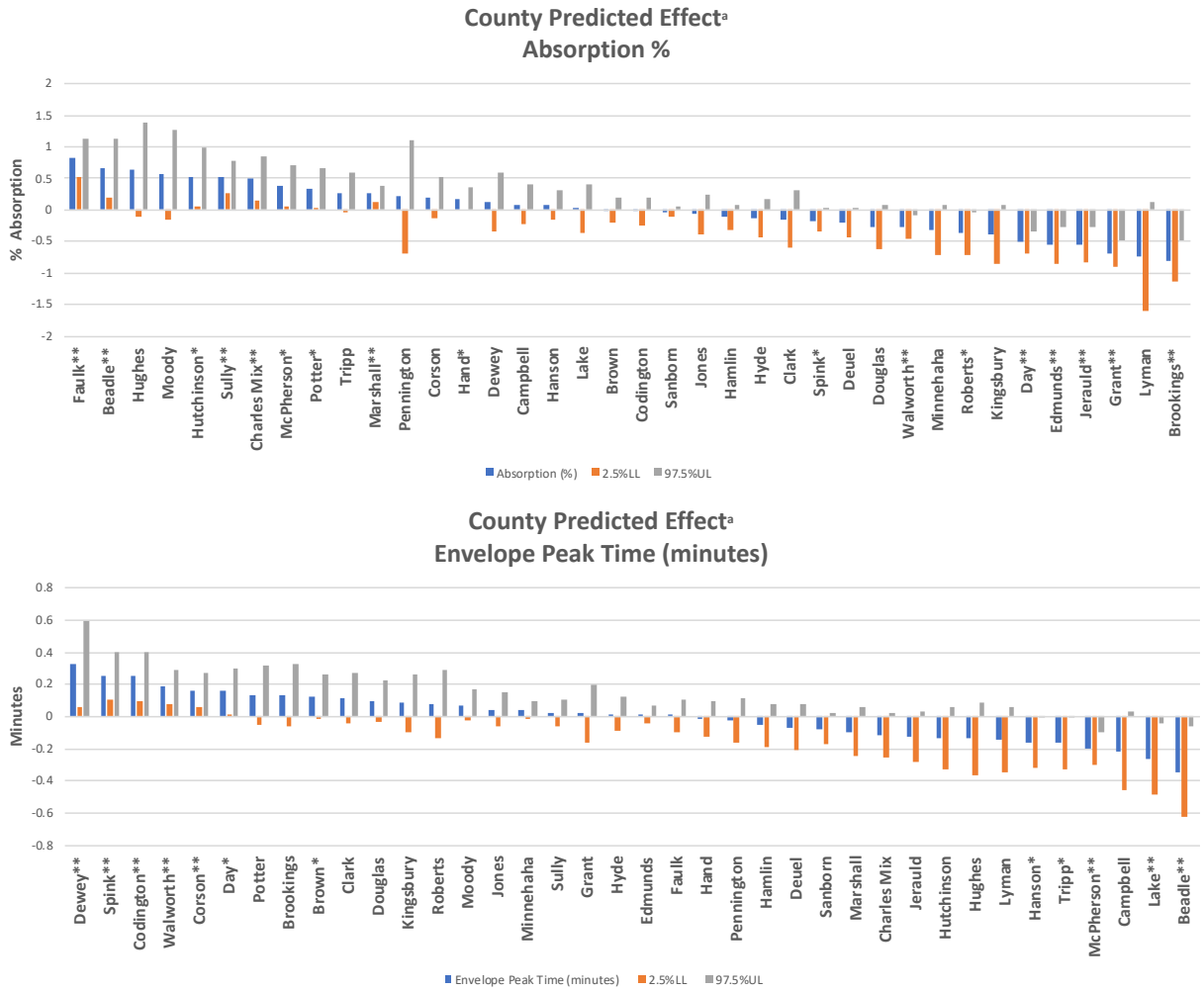



*Figure 3.13. County predicted effect for absorption and envelope peak time, respectively, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

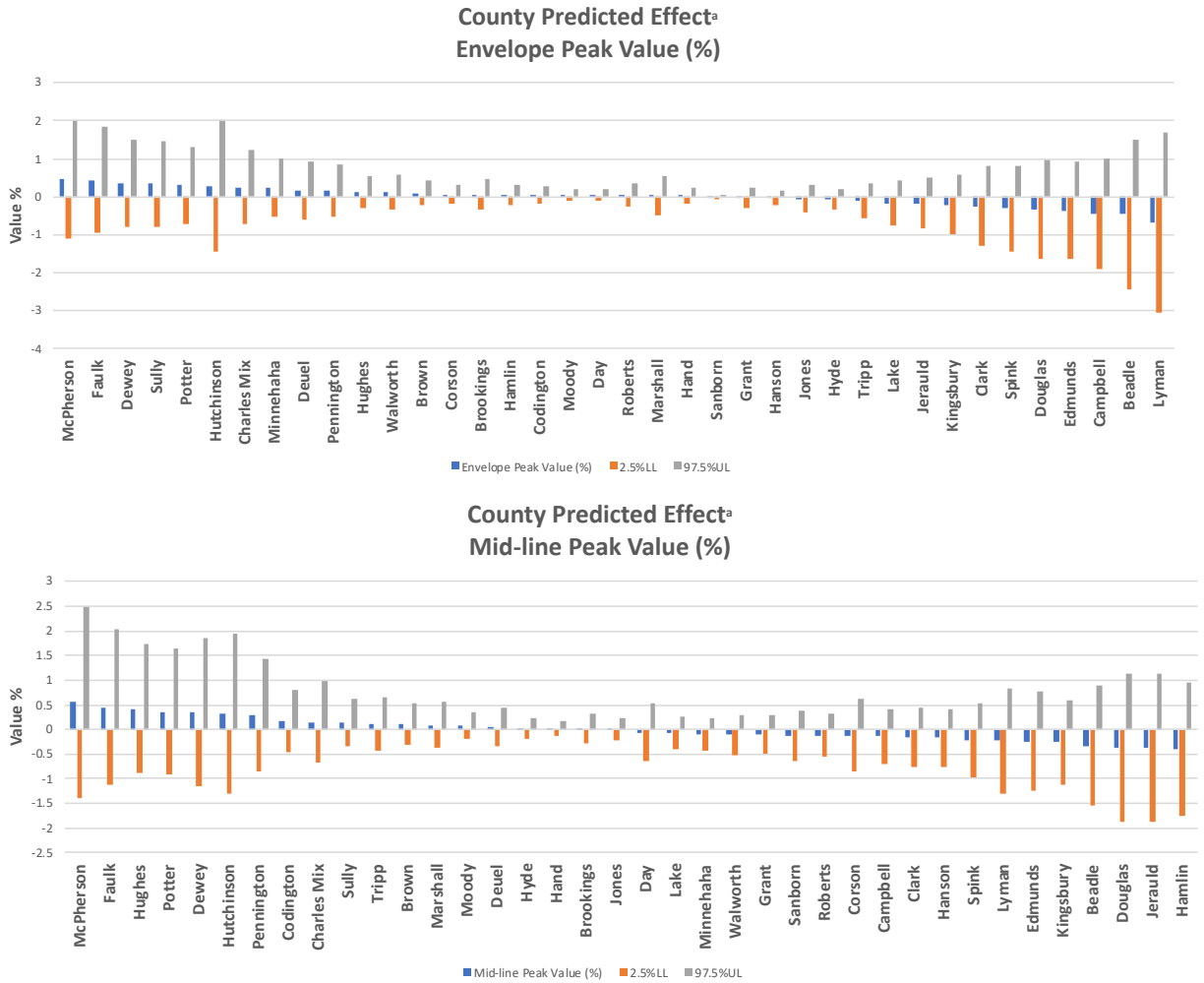



*Figure 3.14. County predicted effect for envelope peak value and mid-line peak value, respectively, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

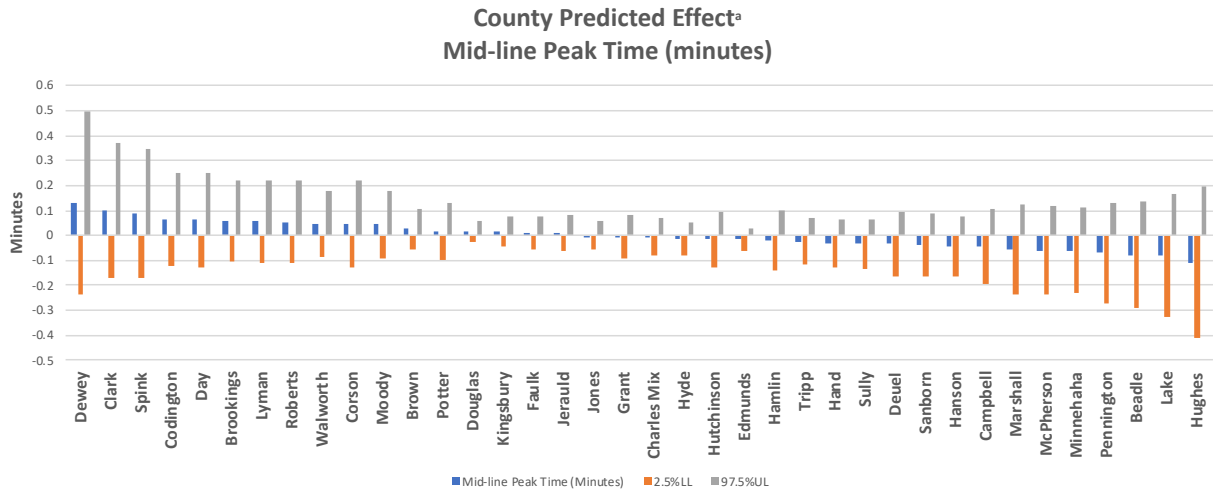



*Figure 3.15. County predicted effect for mid-line peak time, using AUP over analysis years and varieties.*

[a]*, **Correlations significant at P < 0.05 and P < 0.01, respectively.
LL and UL: lower and upper limits of a 95% confidence interval.

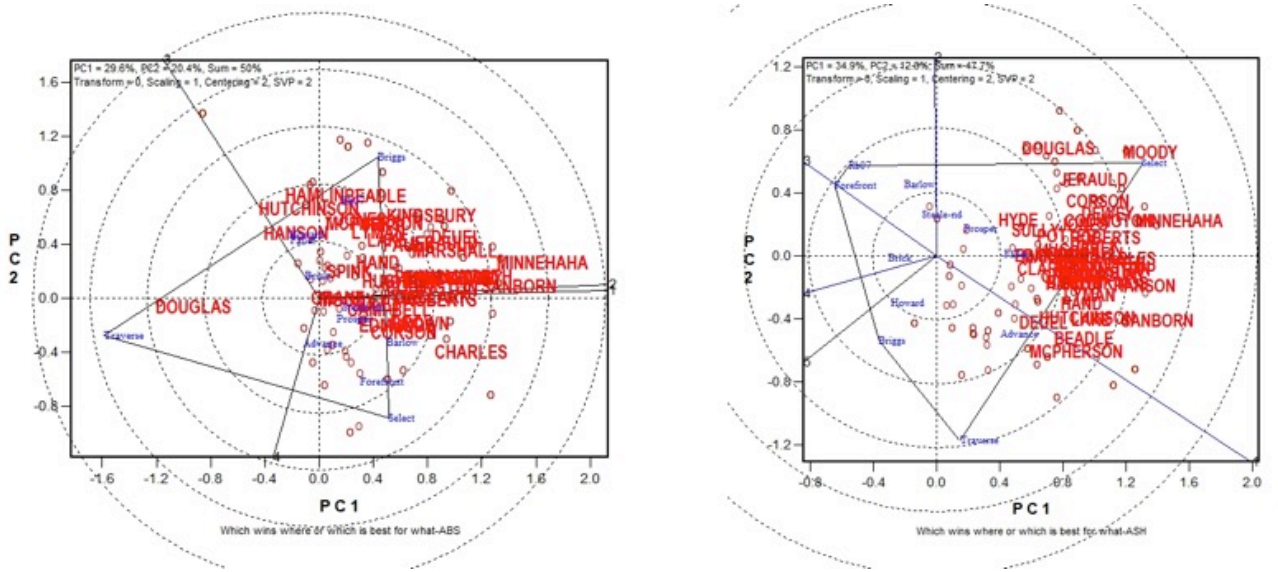



*Figure 3.16. Genotype and mega-location evaluation for absorption and ash content, respectively. Created using GGE biplot software over analysis years.*

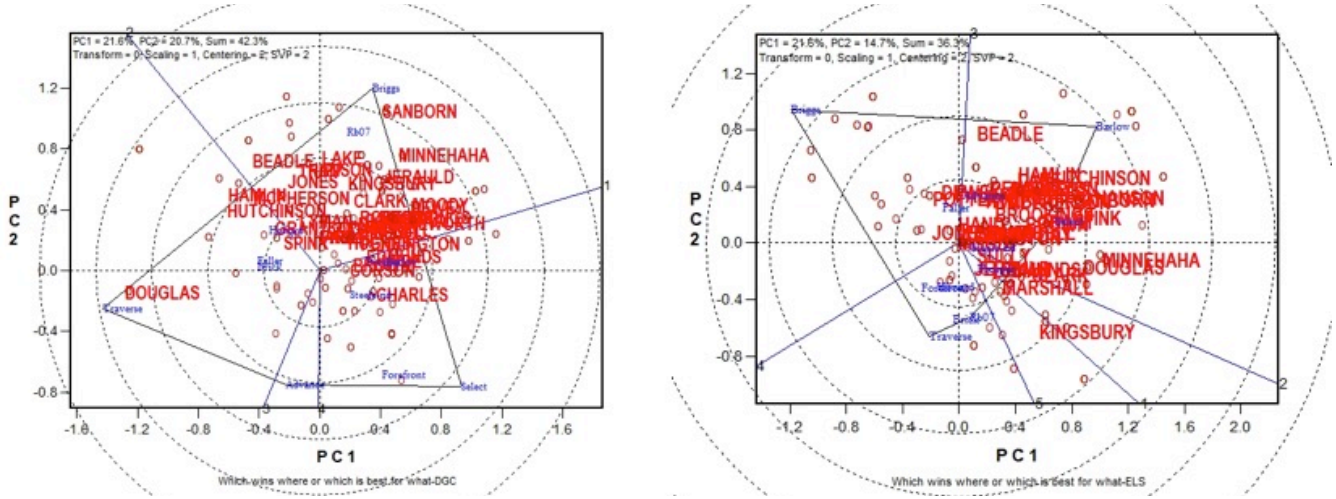



*Figure 3.17. Genotype and mega-location evaluation for dry gluten content and envelope left-of-peak slope, respectively. Created using GGE biplot software over analysis years.*

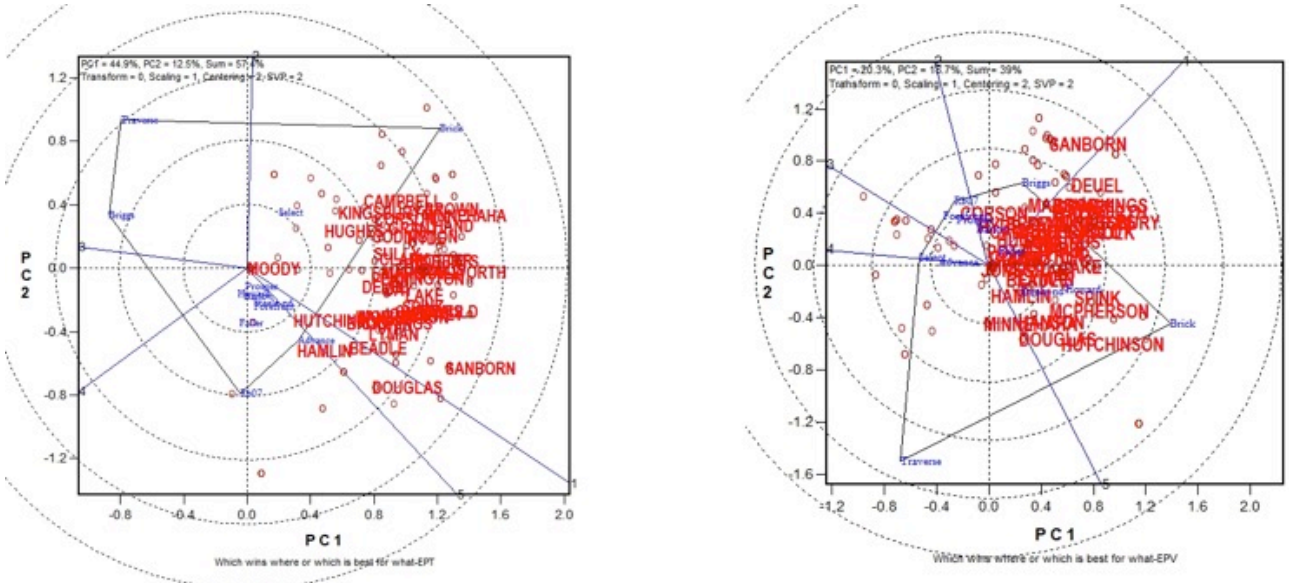



*Figure 3.18. Genotype and mega-location evaluation for envelope peak time and envelope peak value, respectively. Created using GGE biplot software over analysis years.*

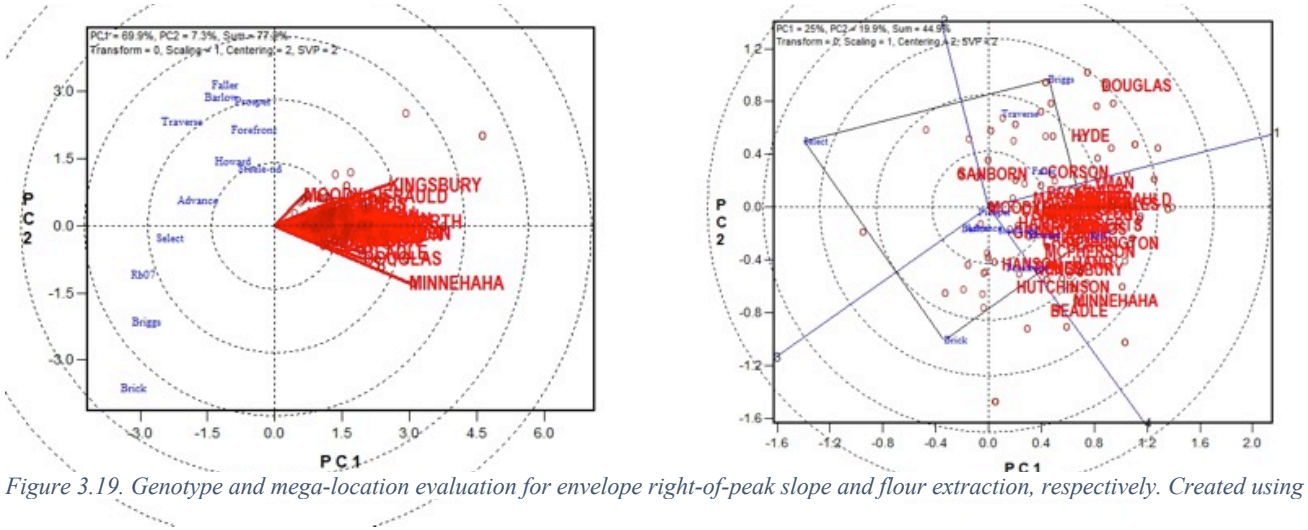



*Figure 3.19. Genotype and mega-location evaluation for envelope right-of-peak slope and flour extraction, respectively. Created using GGE biplot software over analysis years.*

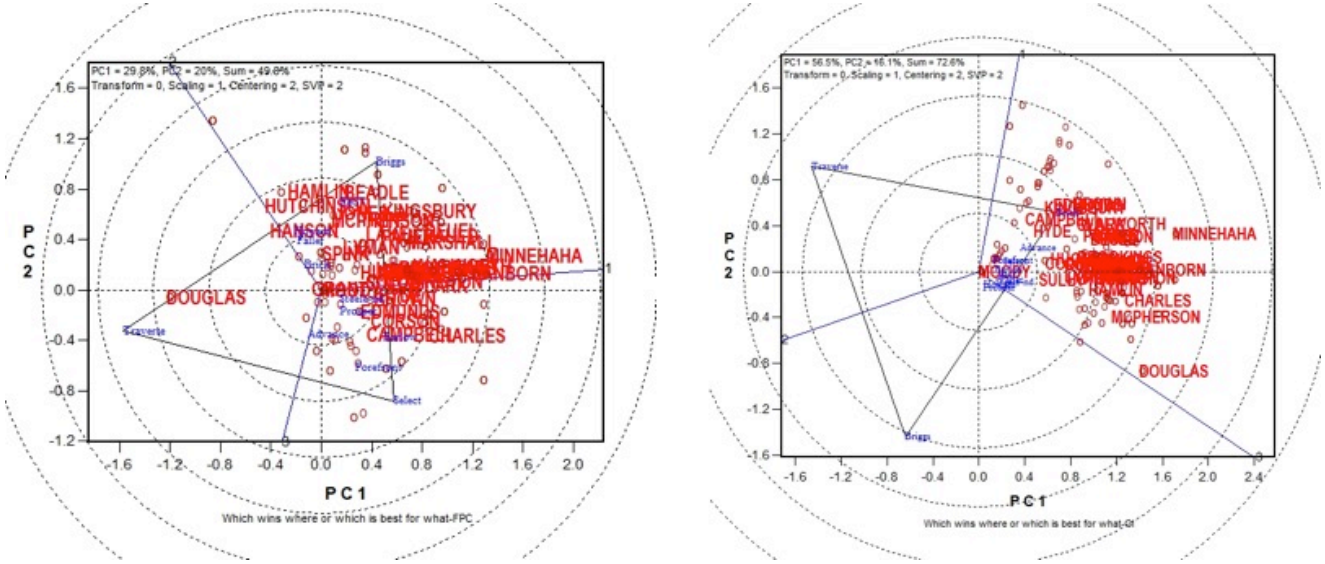



*Figure 3.20. Genotype and mega-location evaluation for flour protein content and gluten index, respectively. Created using GGE biplot software over analysis years.*

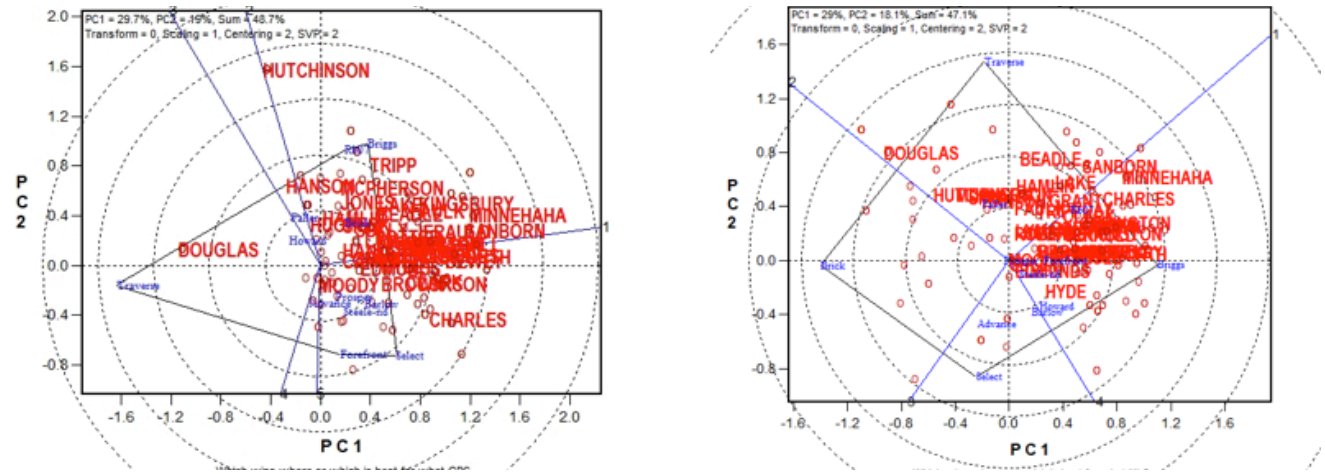
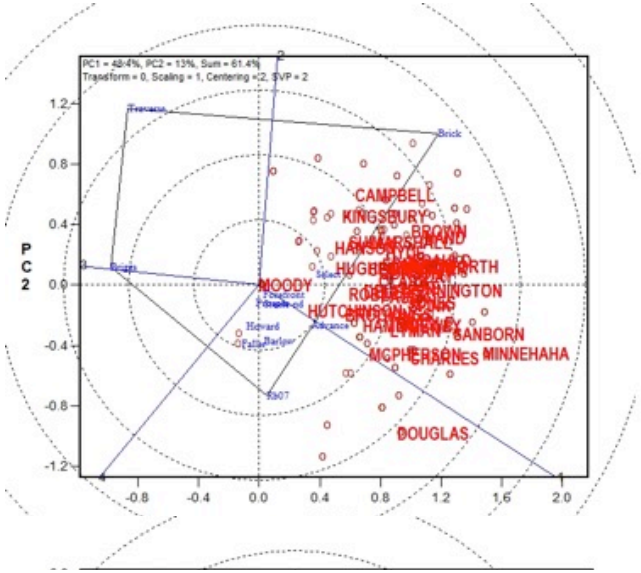



*Figure 3.21. Genotype and mega-location evaluation for grain protein content and mid-line left-of-peak slope, respectively. Created using GGE biplot software over analysis years.*



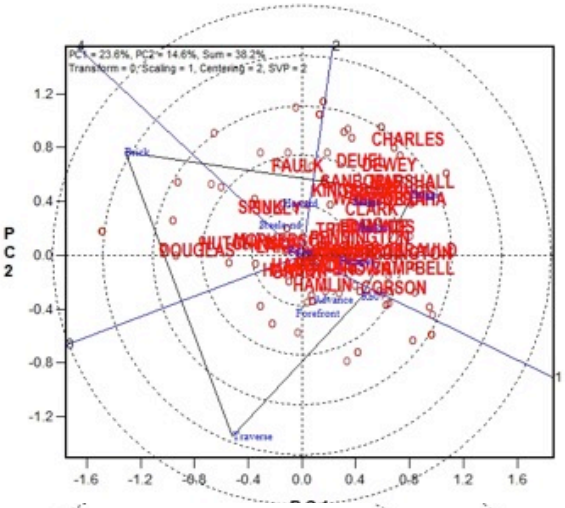
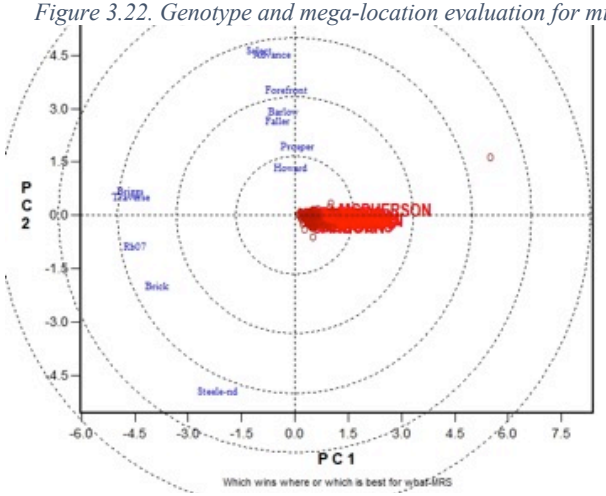




*Figure 3.22. Genotype and mega-location evaluation for mid-line peak time and mid-line peak value, respectively. Created using GGE biplot software over analysis years.*



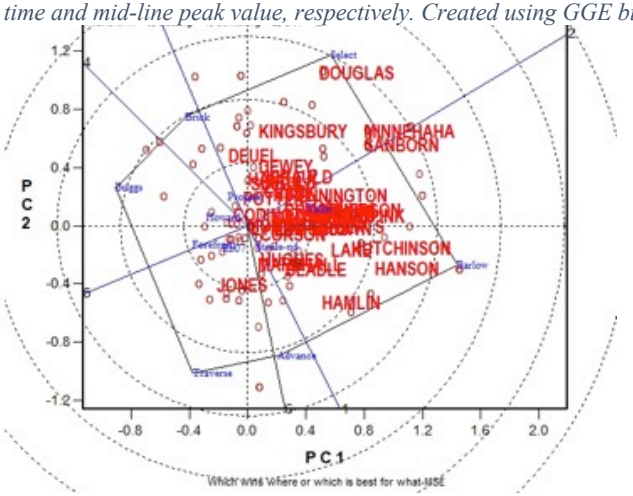




*Figure 3.23. Genotype and mega-location evaluation for mid-line right-of-peak slope and envelope mixing stability, respectively. Created using GGE biplot software over analysis years.*

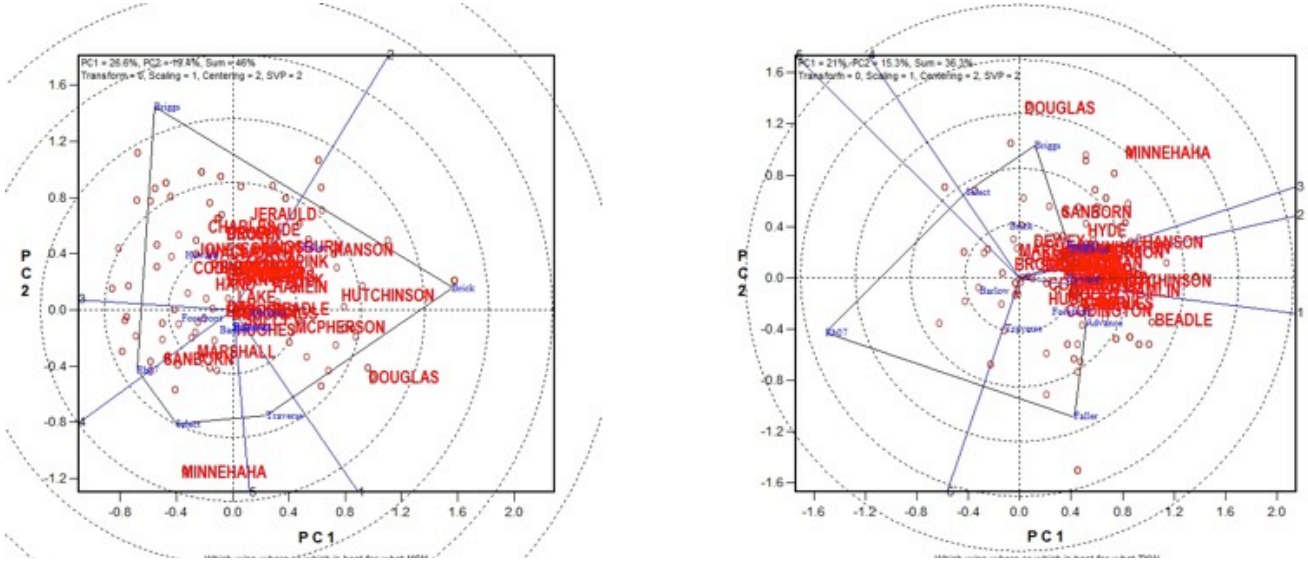



*Figure 3.24. Genotype and mega-location evaluation for mid-line mixing stability and thousand kernel weight, respectively. Created using GGE biplot software over analysis years.*

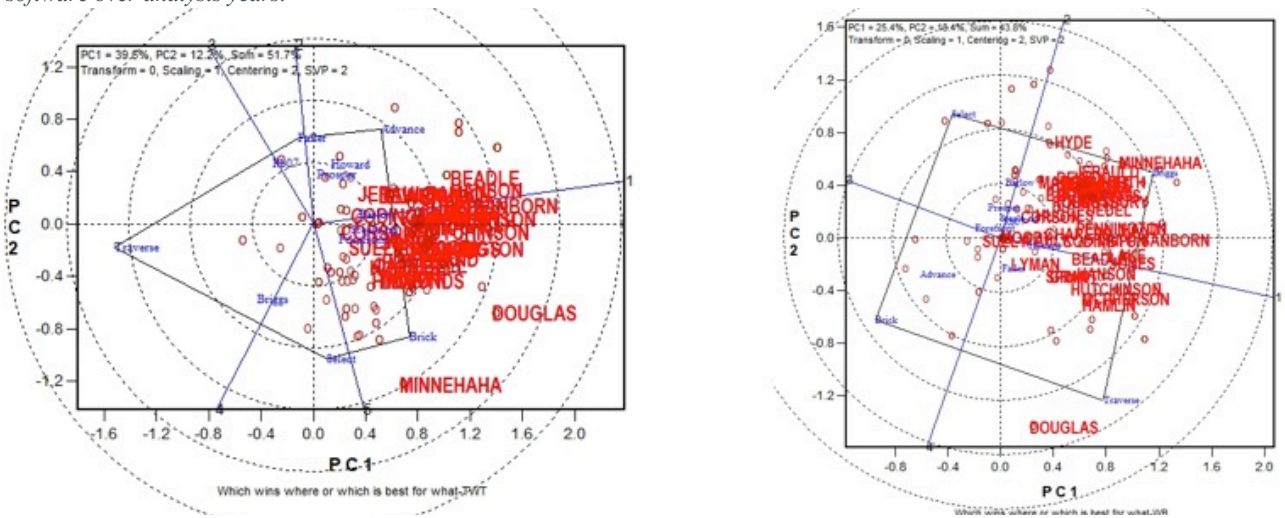



*Figure 3.25. Genotype and mega-location evaluation for thousand kernel weight and water binding, respectively. Created using GGE biplot software over analysis years.*

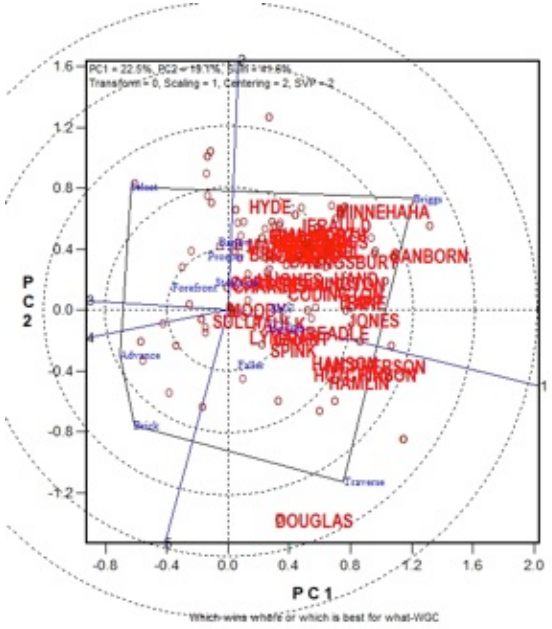



*Figure 3.26. Genotype and mega-location evaluation for wet gluten content. Created using GGE biplot software over analysis years.*

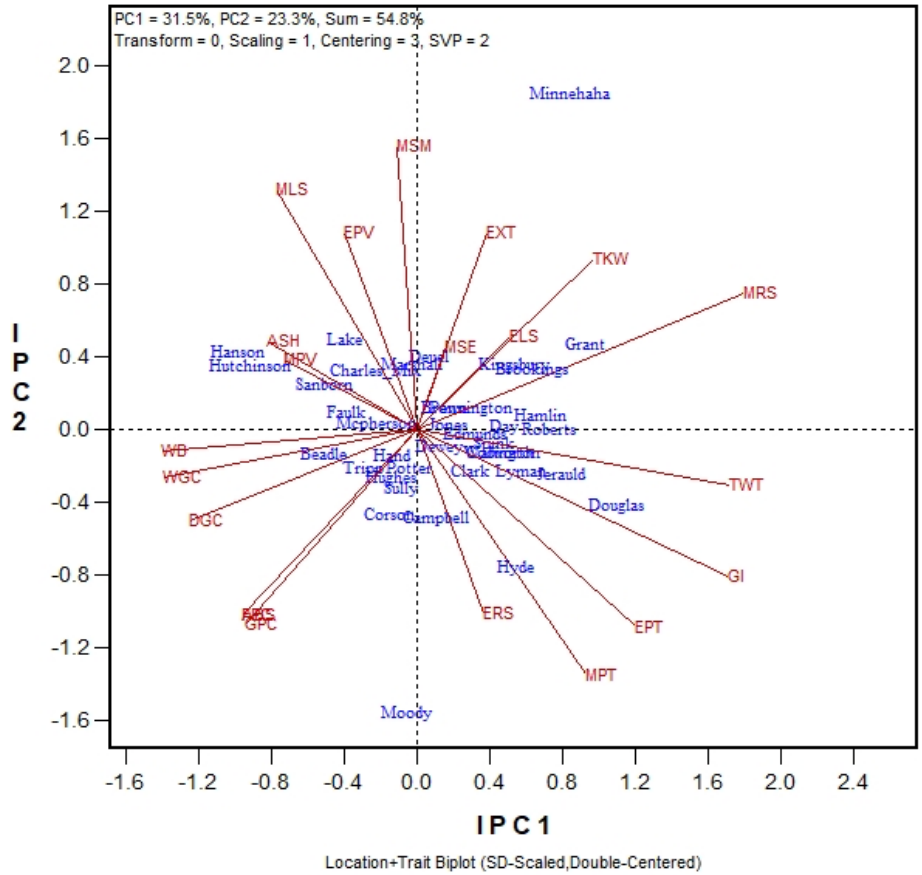



*Figure 3.27. Location + Trait Biplot with Standard Deviation scale and double centered (GE).* *Created using GGE biplot software over analysis years and varieties.*

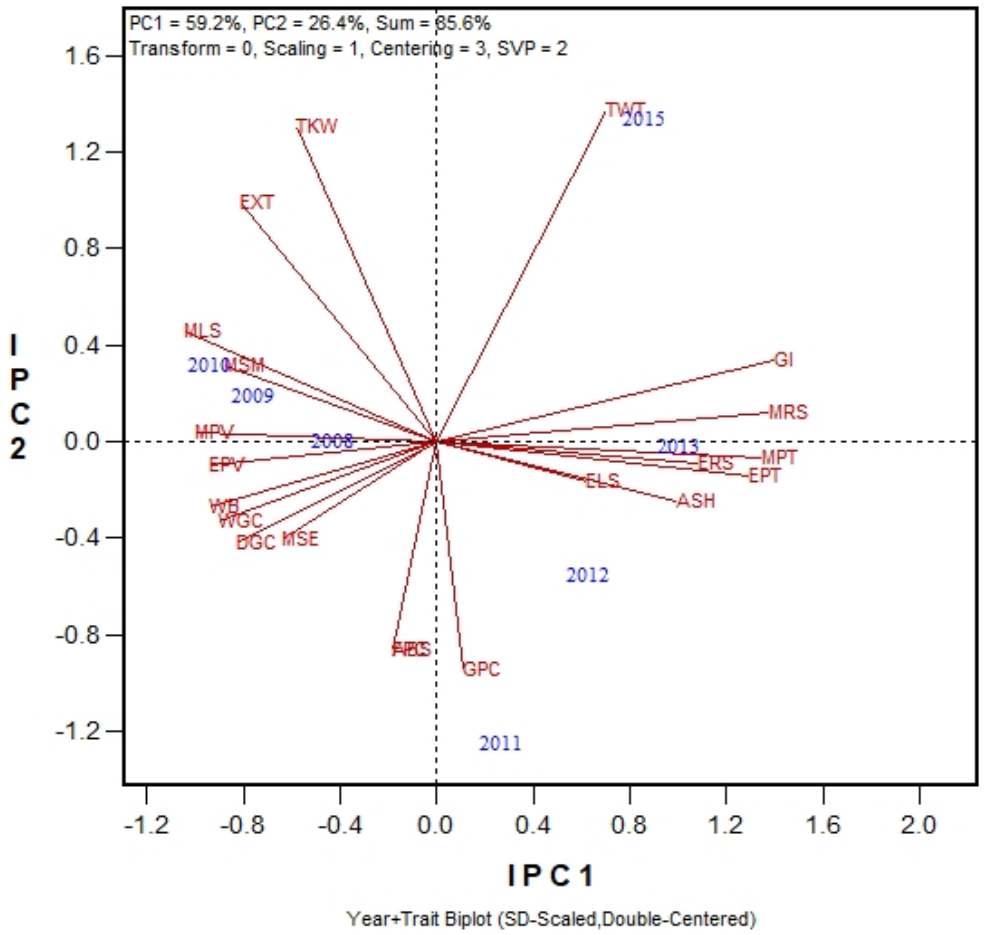



*Figure 3.28. Year + Trait Biplot with Standard Deviation scale and double centered (GE). Created using GGE biplot software over analysis varieties and production environments.*

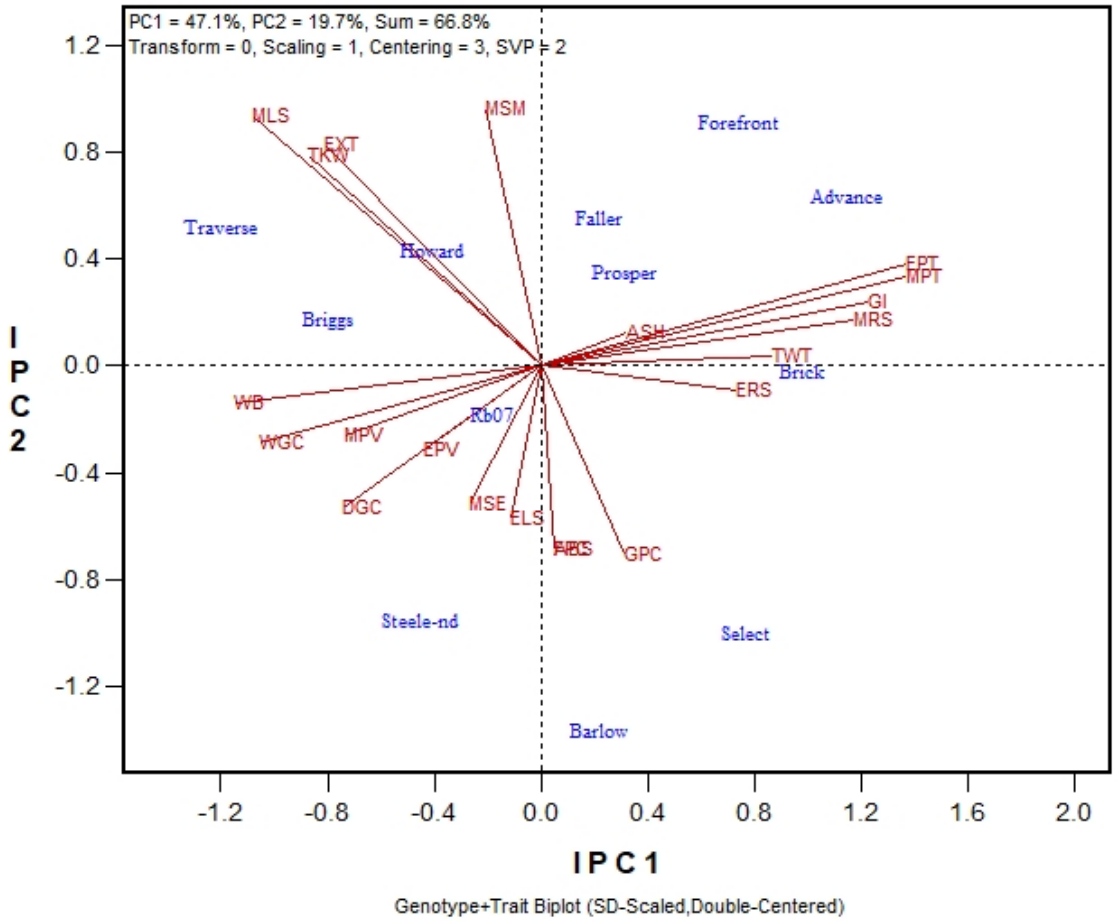



*Figure 3.29. Genotype + Trait Biplot with Standard Deviation scale and double centered (GE). Created using GGE biplot software over analysis years and production environments.*